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(54) Title: TRANSCRIPTION FACTORS

(57) Abstract: The invention provides human transcription factors (TRFX) and polynucleotides which identify and encode TRFX. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of TRFX.

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TRANSCRIPTION FACTORS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of transcription factors and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative, autoimmune/inflammatory, neurological, and developmental disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transcription factors.

BACKGROUND OF THE INVENTION

Multicellular organisms are comprised of diverse cell types that differ dramatically both in structure and function. The identity of a cell is determined by its characteristic pattern of gene expression, and different cell types express overlapping but distinct sets of genes throughout development. Spatial and temporal regulation of gene expression is critical for the control of cell proliferation, cell differentiation, apoptosis, and other processes that contribute to organism development. Furthermore, gene expression is regulated in response to extracellular signals that mediate cell-cell communication and coordinate the activities of different cell types. Appropriate gene regulation also ensures that cells function efficiently by expressing only those genes whose functions are required at a given time.

Transcriptional regulatory proteins are essential for the control of gene expression. Some of these proteins function as transcription factors that initiate, activate, repress, or terminate gene transcription. Transcription factors generally bind to promoter, enhancer, or upstream regulatory regions of a gene in a sequence-specific manner, although some factors bind regulatory elements within or downstream of the coding region. Transcription factors may bind to a specific region of DNA singly or as a complex with other accessory factors. (Reviewed in Lewin, B. (1990) Genes IV, Oxford University Press, New York, NY, pp. 554-570.)

The double helix structure and repeated sequences of DNA create topological and chemical features which can be recognized by transcription factors. These features include hydrogen bond donor and acceptor groups, hydrophobic patches, major and minor grooves, and regular repeated stretches of sequence which induce distinct bends in the helix. Typically, transcription factors recognize specific DNA sequence motifs of about 20 nucleotides in length. Multiple adjacent transcription factor-binding motifs may be required for gene regulation.

Many transcription factors incorporate DNA-binding structural motifs which comprise either α helices or β sheets that bind to the major groove of DNA. Four well-characterized structural motifs are helix-turn-helix, zinc finger, leucine zipper, and helix-loop-helix. Proteins containing these

motifs may act alone as monomers or form homo- or heterodimers that interact with DNA.

The zinc finger motif, which binds zinc ions, generally contains tandem repeats of about 30 amino acids consisting of periodically spaced cysteine and histidine residues. Examples of this sequence pattern include the C2H2-type and the C3HC4-type zinc fingers, and the PHD domain.

- 5 (Lewin, supra ; Aasland, R., et al. (1995) Trends Biochem. Sci 20:56 - 59.) Zinc finger proteins each contain an α helix and an antiparallel β sheet whose proximity and conformation are maintained by the zinc ion. Contact with DNA is made by the arginine preceding the α helix and by the second, third, and sixth residues of the α helix.

- 10 The leucine zipper motif comprises a stretch of amino acids rich in leucine which can form an amphipathic α helix. This structure provides the basis for dimerization of two leucine zipper proteins. The region adjacent to the leucine zipper is usually basic, and upon protein dimerization, is optimally positioned for binding to the major groove. Proteins containing such motifs are generally referred to as bZIP transcription factors. The helix-loop-helix motif (HLH) consists of a short α helix connected by a loop to a longer α helix. The loop is flexible and allows the two helices to fold back
15 against each other and to bind to DNA. The transcription factor Myc contains a prototypical HLH motif. Most transcription factors contain characteristic DNA binding motifs, and variations on the above motifs and new motifs have been and are currently being characterized (Faisst, S. and S. Meyer (1992) Nucl. Acids Res. 20:3-26).

- 20 Mutations in transcription factors contribute to oncogenesis. This is likely due to the role of transcription factors in the expression of genes involved in cell proliferation. For example, mutations in transcription factors encoded by proto-oncogenes, such as Fos, Jun, Myc, Rel, and Spi1, may be oncogenic due to increased stimulation of cell proliferation. Conversely, mutations in transcription factors encoded by tumor suppressor genes, such as p53, RB1, and WT1, may be oncogenic due to decreased inhibition of cell proliferation. (Latchman, D. (1995) Gene Regulation: A Eukaryotic
25 Perspective, Chapman and Hall, London, UK, pp 242-255.)

- Gene expression is also affected by chromatin-associated proteins. In the nucleus, DNA is packaged into chromatin, the compact organization of which limits the accessibility of DNA to transcription factors and plays a key role in gene regulation. (Lewin, supra, pp. 409-410.) The compact structure of chromatin is determined and influenced by chromatin-associated proteins such
30 as histones, high mobility group (HMG) proteins, helicases, and chromodomain proteins. There are five classes of histones, H1, H2A, H2B, H3, and H4, all of which are highly basic, low molecular weight proteins. The fundamental unit of chromatin, the nucleosome, consists of 200 base pairs of DNA associated with two copies each of H2A, H2B, H3, and H4. H1 links adjacent nucleosomes. HMG proteins are low molecular weight, non-histone proteins that may play a role in unwinding

DNA and stabilizing single-stranded DNA. Helicases, which are DNA-dependent ATPases, unwind DNA, allowing access for transcription factors. Chromodomain proteins play a key role in the formation of highly-compacted, transcriptionally silent heterochromatin.

Many neoplastic disorders in humans can be attributed to inappropriate gene expression.

5 Malignant cell growth may result from either excessive expression of tumor promoting genes or insufficient expression of tumor suppressor genes. (Cleary, M.L. (1992) *Cancer Surv.* 15:89-104.) Chromosomal translocations may also produce chimeric loci which fuse the coding sequence of one gene with the regulatory regions of a second unrelated gene. Such an arrangement often results in inappropriate gene transcription. The Wilms tumor suppressor gene product, WT1, is a protein
10 containing a DNA-binding domain consisting of four zinc fingers and a proline-glutamine rich region capable of regulating transcription. (ExPASy PROSITE document PR00049.) Deletions of the WT1 gene, or point mutations which destroy the DNA-binding activity of the protein are associated with development of the pediatric nephroblastoma, Wilms tumor, and Denys-Drash syndrome. (Rauscher, F.J. (1993) *FASEB J.* 7:896-903.)

15 Certain proteins enriched in glutamine are associated with various neurological disorders including spinocerebellar ataxia, bipolar effective disorder, schizophrenia, and autism. (Margolis, R.L. et al. (1997) *Human Genetics* 100:114-122.) These proteins contain regions with as many as 15 or more consecutive glutamine residues and may function as transcription factors with a potential role in regulation of neurodevelopment or neuroplasticity.

20 The immune system responds to infection or trauma by activating a cascade of events that coordinate the progressive selection, amplification, and mobilization of cellular defense mechanisms. A complex and balanced program of gene activation and repression is involved in this process. Hyperactivity of the immune system as a result of improper or insufficient regulation of gene expression may result in considerable tissue or organ damage. This damage is well documented in
25 immunological responses associated with arthritis, allergens, heart attack, stroke, and infections. (*Harrison's Principles of Internal Medicine*, 13/e, McGraw Hill, Inc. and Teton Data Systems Software, 1996.) In particular, a zinc finger protein termed Staf50 (for Stimulated trans-acting factor of 50 kDa) is a transcriptional regulator and is induced in various cell lines by interferon-I and -II. Staf50 appears to mediate the antiviral activity of interferon by down-regulating the viral
30 transcription directed by the long terminal repeat promoter region of human immunodeficiency virus type-1 in transfected cells (Tissot, C. (1995) *J. Biol. Chem.* 270:14891-14898).

The generation of multicellular organisms is based on the induction and coordination of cell differentiation at the appropriate stages of development. Differential gene expression confers the distinct identities of cells and tissues throughout the body. Failure to regulate gene expression during

development could result in developmental disorders.

The discovery of new transcription factors and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cell proliferative, autoimmune/inflammatory, neurological, and developmental disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of transcription factors.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, transcription factors, referred to collectively as "TRFX" and individually as "TRFX-1," "TRFX-2," "TRFX-3," "TRFX-4," "TRFX-5," "TRFX-6," "TRFX-7," "TRFX-8," "TRFX-9," "TRFX-10," "TRFX-11," "TRFX-12," "TRFX-13," "TRFX-14," "TRFX-15," "TRFX-16," "TRFX-17," "TRFX-18," "TRFX-19," "TRFX-20," "TRFX-21," "TRFX-22," "TRFX-23," "TRFX-24," "TRFX-25," "TRFX-26," "TRFX-27," "TRFX-28," "TRFX-29," "TRFX-30," "TRFX-31," "TRFX-32," "TRFX-33," "TRFX-34," "TRFX-35," "TRFX-36," "TRFX-37," "TRFX-38," "TRFX-39," "TRFX-40," "TRFX-41," "TRFX-42," "TRFX-43," "TRFX-44," "TRFX-45," "TRFX-46," "TRFX-47," "TRFX-48," "TRFX-49," "TRFX-50," "TRFX-51," "TRFX-52," "TRFX-53," "TRFX-54," "TRFX-55," "TRFX-56," "TRFX-57," "TRFX-58," "TRFX-59," "TRFX-60," "TRFX-61," "TRFX-62," "TRFX-63," "TRFX-64," "TRFX-65," "TRFX-66," "TRFX-67," "TRFX-68," "TRFX-69," "TRFX-70," "TRFX-71," "TRFX-72," "TRFX-73," "TRFX-74," "TRFX-75," "TRFX-76," "TRFX-77," "TRFX-78," "TRFX-79," "TRFX-80," "TRFX-81," "TRFX-82," "TRFX-83," "TRFX-84," "TRFX-85," "TRFX-86," "TRFX-87," "TRFX-88," "TRFX-89," "TRFX-90," "TRFX-91," "TRFX-92," "TRFX-93," "TRFX-94," "TRFX-95," "TRFX-96," "TRFX-97," "TRFX-98," "TRFX-99," "TRFX-100," "TRFX-101," "TRFX-102," "TRFX-103," "TRFX-104," "TRFX-105," "TRFX-106," and "TRFX-107." In one aspect, the invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-107.

The invention further provides an isolated polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having

at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. In one alternative, the polynucleotide
5 encodes a polypeptide selected from the group consisting of SEQ ID NO:1-107. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:108-214.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group
10 consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. In one alternative, the invention provides a cell transformed
15 with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having at least 90%
20 sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant
25 polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring
30 amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107.

The invention further provides an isolated polynucleotide comprising a polynucleotide
35 sequence selected from the group consisting of a) a polynucleotide sequence selected from the group

consisting of SEQ ID NO:108-214, b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide
5 comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, b) a naturally occurring polynucleotide sequence having at least
10 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence complementary to b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to
15 said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, c) a polynucleotide sequence complementary to a), d) a polynucleotide sequence
25 complementary to b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid
30 sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and a
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pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional TRFX, comprising administering to a patient in need of such treatment the composition.

5 The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional TRFX, comprising administering to a patient in need of such treatment the composition.

 Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional TRFX, comprising administering to a patient in need of such treatment the composition.

 The invention further provides a method of screening for a compound that specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence

selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. The method comprises a) combining the polypeptide with at least one test compound
5 under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide comprising an amino acid sequence selected from the group consisting of a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, b) a naturally
10 occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107. The method comprises a) combining the polypeptide with at least one test compound
15 under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

20 The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:108-214, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

25 The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID
30 NO:108-214, ii) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological

sample, said target polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, ii) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214, iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding TRFX.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods, algorithms, and searchable databases used for analysis of TRFX.

Table 3 shows the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis; diseases, disorders, or conditions associated with these tissues; and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding TRFX were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a

reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"TRFX" refers to the amino acid sequences of substantially purified TRFX obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of TRFX. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TRFX either by directly interacting with TRFX or by acting on components of the biological pathway in which TRFX participates.

An "allelic variant" is an alternative form of the gene encoding TRFX. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding TRFX include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as TRFX or a polypeptide with at least one functional characteristic of TRFX. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding TRFX, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding TRFX. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent TRFX. Deliberate amino acid substitutions may be made on the basis of similarity in

polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of TRFX is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of TRFX. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of TRFX either by directly interacting with TRFX or by acting on components of the biological pathway in which TRFX participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind TRFX polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic TRFX, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding TRFX or fragments of TRFX may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

"Conservative amino acid substitutions" are those substitutions that are predicted to least

interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

5	<u>Original Residue</u>	<u>Conservative Substitution</u>
	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
10	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
15	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
20	Ser	Cys, Thr
	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
25	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

A "fragment" is a unique portion of TRFX or the polynucleotide encoding TRFX which is

identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50% of a polypeptide) as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:108-214 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:108-214, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:108-214 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:108-214 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:108-214 and the region of SEQ ID NO:108-214 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-107 is encoded by a fragment of SEQ ID NO:108-214. A fragment of SEQ ID NO:1-107 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-107. For example, a fragment of SEQ ID NO:1-107 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-107. The precise length of a fragment of SEQ ID NO:1-107 and the region of SEQ ID NO:1-107 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full-length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full-length" polynucleotide sequence encodes a "full-length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and

therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at

<http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous

nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

5 Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

10 The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

15 Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by
20 CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.12 (Apr-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

25 *Matrix: BLOSUM62*
 Open Gap: 11 and Extension Gap: 1 penalties
 Gap x drop-off: 50
 Expect: 10
 Word Size: 3
30 *Filter: on*

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least
35 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment

length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term “humanized antibody” refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular

circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

5 The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate
10 to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression
15 of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of TRFX which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment
20 of TRFX which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other
25 chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of TRFX. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of TRFX.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide,
30 polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably
35 linked to a coding sequence if the promoter affects the transcription or expression of the coding

sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

“Post-translational modification” of an TRFX may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of TRFX.

“Probe” refers to nucleic acid sequences encoding TRFX, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule.

Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes.

“Primers” are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to

100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription,

translation, or RNA stability.

“Reporter molecules” are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and
5 other moieties known in the art.

An “RNA equivalent,” in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

10 The term “sample” is used in its broadest sense. A sample suspected of containing nucleic acids encoding TRFX, or fragments thereof, or TRFX itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms “specific binding” and “specifically binding” refer to that interaction between a
15 protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope “A,” the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A
20 and the antibody will reduce the amount of labeled A that binds to the antibody.

The term “substantially purified” refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

25 A “substitution” refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

“Substrate” refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells,
30 trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A “transcript image” refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

“Transformation” describes a process by which exogenous DNA is introduced into a recipient
cell. Transformation may occur under natural or artificial conditions according to various methods
35 well known in the art, and may rely on any known method for the insertion of foreign nucleic acid

sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term “transformed” cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A “transgenic organism,” as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants, and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook, J. et al. (1989), supra.

A “variant” of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the “BLAST 2 Sequences” tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95% or at least 98% or greater sequence identity over a certain defined length. A variant may be described as, for example, an “allelic” (as defined above), “splice,” “species,” or “polymorphic” variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass “single nucleotide polymorphisms” (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a

propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 98% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

The invention is based on the discovery of new human transcription factors (TRFX), the polynucleotides encoding TRFX, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative, autoimmune/inflammatory, neurological, and developmental disorders.

Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding TRFX. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte clones in which nucleic acids encoding each TRFX were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. In some cases, GenBank sequence identifiers are also shown in column 5. The Incyte clones and GenBank cDNA sequences, where indicated, in column 5 were used to assemble the consensus nucleotide sequence of each TRFX and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO and Incyte clone ID of each polypeptide; column 2 shows the number of amino acid residues in each polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows homologous sequences as identified by BLAST analysis along with relevant citations, all of which are expressly incorporated by reference herein in their entirety; and column 7 shows analytical methods and in some cases, searchable databases to which the analytical methods were applied. The methods of column 7 were used to characterize each polypeptide through sequence homology and protein motifs.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding TRFX. The first column of Table 3 lists the nucleotide SEQ ID NOs and Incyte Clone IDs. Fragments of these polynucleotides are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:108-214 and to distinguish between SEQ ID NO:108-214 and related polynucleotide sequences. The polypeptides

encoded by these fragments are useful, for example, as immunogenic peptides. Column 2 lists tissue categories which express TRFX as a fraction of total tissues expressing TRFX. Column 3 lists diseases, disorders, or conditions associated with those tissues expressing TRFX as a fraction of total tissues expressing TRFX. Column 4 lists the vectors used to subclone each cDNA library.

5 The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding TRFX were isolated. Column 1 references the nucleotide SEQ ID NOs and Incyte Clone IDs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

10 SEQ ID NO:111 maps to chromosome 6 within the interval from 89.4 to 96.1 centiMorgans.
 SEQ ID NO:114 maps to chromosome 6 within the interval from 42.0 to 44.9 centiMorgans.
 SEQ ID NO:117 maps to chromosome 13 within the interval from 95.9 to 112.7 centiMorgans.

 SEQ ID NO:122 maps to chromosome 3 within the interval from 55.4 to 63.3 centiMorgans.
 15 SEQ ID NO:123 maps to chromosome 7 within the interval from 149.6 to 159.0 centiMorgans.
 SEQ ID NO:125 maps to chromosome 15 within the interval from 45.5 to 58.8 centiMorgans.
 SEQ ID NO:130 maps to chromosome 1 within the interval from 152.2 to 156.1 centiMorgans.

20 SEQ ID NO:132 maps to chromosome 1 within the interval from 36.2 to 54.2 centiMorgans.
 SEQ ID NO:133 maps to chromosome 19 within the interval from 41.7 to 49.4 centiMorgans.
 SEQ ID NO:134 maps to chromosome 17 within the interval from 99.3 to 104.7 centiMorgans.

 SEQ ID NO:136 maps to chromosome 16 within the interval from 119.2 centiMorgans to the
 25 q-terminus.

 SEQ ID NO:138 maps to chromosome 19 within the interval from 60.9 to 61.4 centiMorgans.
 SEQ ID NO:145 maps to chromosome 2 within the interval from 190.8 to 196.8 centiMorgans and to chromosome 10 within the interval from 68.7 to 72.5 centiMorgans.
 SEQ ID NO:149 maps to chromosome 3 within the interval from the p terminus to 16.5
 30 centiMorgans.

 SEQ ID NO:152 maps to chromosome 19 within the interval from 35.5 to 49.4 centiMorgans and to chromosome 7 within the interval from 100.5 to 114.5 centiMorgans and to chromosome 7 within the intervals from 67.6 to 69.3 centiMorgans and 83.8 centiMorgans and the q-terminus.

 SEQ ID NO:153 maps to chromosome 16 within the interval from 65.6 to 72.6 centiMorgans.
 35 SEQ ID NO:156 maps to chromosome 20 within the interval from 65.5 to 79.0 centiMorgans.

SEQ ID NO:159 maps to chromosome 18 within the interval from 40.4 to 49.7 centiMorgans.

SEQ ID NO:168 maps to chromosome 23 within the interval from 112.8 to 139.4

centiMorgans.

SEQ ID NO:179 maps to chromosome 11 within the interval from 16.7 to 24.7 centiMorgans.

5 SEQ ID NO:180 maps to chromosome 16 within the interval from 33.3 to 42.7 centiMorgans

SEQ ID NO:184 maps to chromosome 2 within the interval from 190.5 to 196.8

centiMorgans and within the interval from the p terminus to 16.4 centiMorgans.

SEQ ID NO:185 maps to chromosome 9 within the interval from 20.4 to 27.8 centiMorgans

and from the p terminus to 33.3 centiMorgans.

10 SEQ ID NO:196 maps to chromosome 1 within the interval from 57.2 to 57.5 centiMorgans.

SEQ ID NO:197 maps to chromosome 19 within the interval from 60.9 to 61.4 centiMorgans.

SEQ ID NO:199 maps to chromosome 13 within the interval from 77.1 to 86.9 centiMorgans

and to chromosome 2 within the interval from 51.2 to 51.8 centiMorgans.

SEQ ID NO:201 maps to chromosome 22 within the interval from 22.2 to 40.2 centiMorgans.

15 SEQ ID NO:204 maps to chromosome 5 within the interval from 132.8 to 141.4

centiMorgans.

SEQ ID NO:208 maps to chromosome 13 within the interval from 37.3 to 45.8 centiMorgans

and to chromosome 19 within the interval from 58.1 to 58.7 centiMorgans.

SEQ ID NO:212 maps to chromosome 19 within the interval from the p terminus to 35.5

20 centiMorgans and to chromosome 20 within the interval from 50.2 to 53.6.

SEQ ID NO:213 maps to chromosome 6 within the interval from the p terminus to 14.2

centiMorgans.

The invention also encompasses TRFX variants. A preferred TRFX variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid

25 sequence identity to the TRFX amino acid sequence, and which contains at least one functional or structural characteristic of TRFX.

The invention also encompasses polynucleotides which encode TRFX. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:108-214, which encodes TRFX. The polynucleotide

30 sequences of SEQ ID NO:108-214, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding TRFX. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at

35 least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide

sequence encoding TRFX. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:108-214 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:108-214. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of TRFX.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding TRFX, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring TRFX, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode TRFX and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring TRFX under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding TRFX or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding TRFX and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode TRFX and TRFX derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding TRFX or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:108-214 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding TRFX may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) *PCR Methods Applic.* 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) *Nucleic Acids Res.* 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) *PCR Methods Applic.* 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) *Nucleic Acids Res.* 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of

about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode TRFX may be cloned in recombinant DNA molecules that direct expression of TRFX, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express TRFX.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter TRFX-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of TRFX, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired

properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding TRFX may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.) Alternatively, TRFX itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of TRFX, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active TRFX, the nucleotide sequences encoding TRFX or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding TRFX. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding TRFX. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding TRFX and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be

provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

5 Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding TRFX and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding TRFX. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); 15 plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; 20 Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184; Engelhard, E.K. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945; Takamatsu, N. (1987) *EMBO J.* 6:307-311; Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 25 191-196; Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659; and Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) *Cancer Gen. Ther.* 5(6):350-356; Yu, M. et al. (1993) *Proc. Natl. Acad. Sci. USA* 90(13):6340-6344; Buller, R.M. et al. (1985) *Nature* 317(6040):813-815; McGregor, D.P. et al. 30 (1994) *Mol. Immunol.* 31(3):219-226; and Verma, I.M. and N. Somia (1997) *Nature* 389:239-242.) The invention is not limited by the host cell employed.

— In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding TRFX. For example, routine cloning, 35 subcloning, and propagation of polynucleotide sequences encoding TRFX can be achieved using a

multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding TRFX into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for

5 in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of TRFX are needed, e.g. for the production of antibodies, vectors which direct high level expression of TRFX may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

10 Yeast expression systems may be used for production of TRFX. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel,

15 1995, supra; Bitter, supra; and Scorer, supra.)

Plant systems may also be used for expression of TRFX. Transcription of sequences encoding TRFX may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock

20 promoters may be used. (See, e.g., Coruzzi, supra; Broglie, supra; and Winter, supra.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases

25 where an adenovirus is used as an expression vector, sequences encoding TRFX may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses TRFX in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma

30 virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino

35 polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet.

15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of TRFX in cell lines is preferred. For example, sequences encoding TRFX can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous
5 expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using
10 tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* and *ap^r* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic,
15 or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which
20 alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system.
25 (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding TRFX is inserted within a marker gene sequence, transformed cells containing sequences encoding TRFX can be identified by the absence of marker gene function. Alternatively, a
30 marker gene can be placed in tandem with a sequence encoding TRFX under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding TRFX and that express TRFX may be identified by a variety of procedures known to those of skill in the art. These
35 procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR

amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of TRFX using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on TRFX is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding TRFX include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding TRFX, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding TRFX may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode TRFX may be designed to contain signal sequences which direct secretion of TRFX through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity.

Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

5 In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding TRFX may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric TRFX protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of TRFX activity. Heterologous protein and
10 peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and
15 metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the TRFX encoding sequence and the heterologous protein sequence, so that TRFX may be cleaved away from the heterologous moiety following purification.
20 Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled TRFX may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These
25 systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

TRFX of the present invention or fragments thereof may be used to screen for compounds that specifically bind to TRFX. At least one and up to a plurality of test compounds may be screened
30 for specific binding to TRFX. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of
--- TRFX, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a
natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2):
35 Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which TRFX

binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express TRFX, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or
5 E. coli. Cells expressing TRFX or cell membrane fractions which contain TRFX are then contacted with a test compound and binding, stimulation, or inhibition of activity of either TRFX or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example,
10 the assay may comprise the steps of combining at least one test compound with TRFX, either in solution or affixed to a solid support, and detecting the binding of TRFX to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a
15 solid support.

TRFX of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of TRFX. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for TRFX activity, wherein TRFX is combined with at least one test compound, and the activity of TRFX in the
20 presence of a test compound is compared with the activity of TRFX in the absence of the test compound. A change in the activity of TRFX in the presence of the test compound is indicative of a compound that modulates the activity of TRFX. Alternatively, a test compound is combined with an in vitro or cell-free system comprising TRFX under conditions suitable for TRFX activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of TRFX
25 may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding TRFX or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal
30 models of human disease. (See, e.g., U.S. Patent No. 5,175,383 and U.S. Patent No. 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host

genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell

5 blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding TRFX may also be manipulated in vitro in ES cells derived from

10 human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding TRFX can also be used to create "knockin" humanized animals

15 (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding TRFX is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease.

20 Alternatively, a mammal inbred to overexpress TRFX, e.g., by secreting TRFX in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of TRFX and transcription factors. In addition, the expression of TRFX is closely

25 associated with reproductive, nervous, and hematopoietic/immune tissues. Therefore, TRFX appears to play a role in cell proliferative, autoimmune/inflammatory, neurological, and developmental disorders. In the treatment of disorders associated with increased TRFX expression or activity, it is desirable to decrease the expression or activity of TRFX. In the treatment of disorders associated with decreased TRFX expression or activity, it is desirable to increase the expression or activity of

30 TRFX.

Therefore, in one embodiment, TRFX or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRFX. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed

connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia,

5 gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-

10 candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or

15 pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a neurological disorder

20 such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess,

25 suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central

30 nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD),

akathesia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; and a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly,

10 craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss.

In another embodiment, a vector capable of expressing TRFX or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRFX including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified TRFX in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRFX including, but not limited to, those provided above.

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In still another embodiment, an agonist which modulates the activity of TRFX may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of TRFX including, but not limited to, those listed above.

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In a further embodiment, an antagonist of TRFX may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TRFX. Examples of such disorders include, but are not limited to, those cell proliferative, autoimmune/inflammatory, neurological, and developmental disorders described above. In one aspect, an antibody which specifically binds TRFX may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express TRFX.

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In an additional embodiment, a vector expressing the complement of the polynucleotide encoding TRFX may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of TRFX including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic

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efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of TRFX may be produced using methods which are generally known in the art. In particular, purified TRFX may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind TRFX. Antibodies to TRFX may also
5 be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans,
10 and others may be immunized by injection with TRFX or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in
15 humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to TRFX have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches
20 of TRFX amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to TRFX may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma
25 technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate
30 antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce TRFX-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be
35 generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g.,

Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA

5 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for TRFX may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and
10 easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such
15 immunoassays typically involve the measurement of complex formation between TRFX and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering TRFX epitopes is generally used, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay
20 techniques may be used to assess the affinity of antibodies for TRFX. Affinity is expressed as an association constant, K_a, which is defined as the molar concentration of TRFX-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple TRFX epitopes, represents the average affinity, or avidity, of the antibodies for
25 TRFX. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular TRFX epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10⁹ to 10¹² L/mole are preferred for use in immunoassays in which the TRFX-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10⁶ to 10⁷ L/mole are preferred for use in immunopurification and similar
30 procedures which ultimately require dissociation of TRFX, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to
35 determine the quality and suitability of such preparations for certain downstream applications. For

example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of TRFX-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g.,

5 Catty, supra, and Coligan et al., supra.)

In another embodiment of the invention, the polynucleotides encoding TRFX, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene
10 encoding TRFX. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding TRFX. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense
15 sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral
20 vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)
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In another embodiment of the invention, polynucleotides encoding TRFX may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined
30 immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) *Science* 270:404-410; Verma, I.M. and N. Somia (1997) *Nature* 389:239-242)), (ii)
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express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in TRFX expression or regulation causes disease, the expression of TRFX from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

- 10 In a further embodiment of the invention, diseases or disorders caused by deficiencies in TRFX are treated by constructing mammalian expression vectors encoding TRFX and introducing these vectors by mechanical means into TRFX-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

- Expression vectors that may be effective for the expression of TRFX include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA),
 20 PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). TRFX may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) Proc. Natl. Acad. Sci. USA
 25 89:5547-5551; Gossen, M. et al. (1995) Science 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and H.M. Blau, supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous
 30 gene encoding TRFX from a normal individual.

- Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method
 35 (Graham, F.L. and A.J. Eb (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al.

(1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to TRFX expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding TRFX under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. USA 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and A.D. Miller (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding TRFX to cells which have one or more genetic abnormalities with respect to the expression of TRFX. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544; and Verma, I.M. and N. Somia (1997) Nature 389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding TRFX to target cells which have one or more genetic abnormalities with

respect to the expression of TRFX. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing TRFX to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has
5 been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a
10 cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple
15 plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding TRFX to target cells. The biology of the prototypic alphavirus,
20 Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity
25 (e.g., protease and polymerase). Similarly, inserting the coding sequence for TRFX into the alphavirus genome in place of the capsid-coding region results in the production of a large number of TRFX-coding RNAs and the synthesis of high levels of TRFX in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN)
30 indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of TRFX into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of
manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA
35 transfections, and performing alphavirus infections, are well known to those with ordinary skill in the

art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding TRFX.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding TRFX. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine,

queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding TRFX. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased TRFX expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding TRFX may be therapeutically useful, and in the treatment of disorders associated with decreased TRFX expression or activity, a compound which specifically promotes expression of the polynucleotide encoding TRFX may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding TRFX is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an *in vitro* cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding TRFX are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding TRFX. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a *Schizosaccharomyces pombe* gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res.

28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of TRFX, antibodies to TRFX, and mimetics, agonists, antagonists, or inhibitors of TRFX.

The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination

of an effective dose is well within the capability of those skilled in the art.

Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising TRFX or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, TRFX or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example TRFX or fragments thereof, antibodies of TRFX, and agonists, antagonists or inhibitors of TRFX, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art.

Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

5 In another embodiment, antibodies which specifically bind TRFX may be used for the diagnosis of disorders characterized by expression of TRFX, or in assays to monitor patients being treated with TRFX or agonists, antagonists, or inhibitors of TRFX. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for TRFX include methods which utilize the antibody and a label to detect TRFX in human body
10 fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring TRFX, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of TRFX expression. Normal
15 or standard values for TRFX expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibody to TRFX under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of TRFX expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values.
20 Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding TRFX may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of TRFX may be correlated with
25 disease. The diagnostic assay may be used to determine absence, presence, and excess expression of TRFX, and to monitor regulation of TRFX levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding TRFX or closely related molecules may be used to identify nucleic acid sequences which encode TRFX. The specificity of the probe, whether it is
30 made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding TRFX, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50%
35 sequence identity to any of the TRFX encoding sequences. The hybridization probes of the subject

invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:108-214 or from genomic sequences including promoters, enhancers, and introns of the TRFX gene.

Means for producing specific hybridization probes for DNAs encoding TRFX include the cloning of polynucleotide sequences encoding TRFX or TRFX derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding TRFX may be used for the diagnosis of disorders associated with expression of TRFX. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and

other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; and a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss. The polynucleotide sequences encoding TRFX may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered TRFX expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding TRFX may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding TRFX may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding TRFX in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of TRFX, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding TRFX, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding TRFX may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding TRFX, or a fragment of a polynucleotide complementary to the polynucleotide encoding TRFX, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding TRFX may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding TRFX are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause

differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of TRFX include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C. et al. (1993) *Anal. Biochem.* 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described in Seilhamer, J.J. et al., "Comparative Gene Transcript Analysis," U.S. Patent No. 5,840,484, incorporated herein by reference. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, antibodies specific for TRFX, or TRFX or fragments thereof may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of

gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by
5 hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

10 Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of
15 pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test
20 compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes
25 are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of
30 Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the
35 treated biological sample are hybridized with one or more probes specific to the polynucleotides of

the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

5 Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under
10 given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson,
15 supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are
20 compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be
25 obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for TRFX to quantify the levels of TRFX expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) Anal. Biochem. 270:103-
30 111; Mendoze, L.G. et al. (1999) Biotechniques 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and
35 should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor

correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) Electrophoresis 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding TRFX may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs),

yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355; Price, C.M. (1993) *Blood Rev.* 7:127-134; and Trask, B.J. (1991) *Trends Genet.* 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop
5 genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, e.g., Lander, E.S. and D. Botstein (1986) *Proc. Natl. Acad. Sci. USA* 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic
10 map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding TRFX on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as
15 linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely
20 localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) *Nature* 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

25 In another embodiment of the invention, TRFX, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between TRFX and the agent being tested may be measured.

30 Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with TRFX, or fragments thereof, and washed. Bound TRFX is then detected by methods well known in the art. Purified TRFX can
35 also be coated directly onto plates for use in the aforementioned drug screening techniques.

Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding TRFX specifically compete with a test compound for binding TRFX.

5 In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with TRFX.

In additional embodiments, the nucleotide sequences which encode TRFX may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such
10 properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

15 Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in
20 particular U.S. Ser. No. 60/188,986, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some
25 tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

30 Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA
35 purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSORT1 plasmid (Life Technologies), pcDNA2.1 plasmid (Invitrogen, Carlsbad CA), or pINCY plasmid (Incyte Genomics, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as

the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI
5 protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VI.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed
10 using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their
15 entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments were generated using the default
20 parameters specified by the clustal algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST,
25 dynamic programing, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and PFAM to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and
30 were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and Hidden Markov Model (HMM)-based protein family databases such
35 as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene

families. (See, e.g., Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:108-214. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, *supra*, ch. 7; Ausubel, 1995, *supra*, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding TRFX occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous,

reproductive, and urologic. The disease/condition categories included cancer, inflammation, trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in

5 Table 3.

V. Chromosomal Mapping of TRFX Encoding Polynucleotides

The cDNA sequences which were used to assemble SEQ ID NO:108-214 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that
10 matched SEQ ID NO:108-214 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 5). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the
15 assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

The genetic map locations of SEQ ID NO:111, 114, 117, 122, 123, 125, 130, 132-134, 136, 138, 145, 149, 152, 153, 156, 159, 168, 179, 180, 184, 185, 196, 197, 199, 201, 204, 208, 212, and 213, are described in The Invention as ranges, or intervals, of human chromosomes. More than one map location is reported for SEQ ID NO:145, 152, 184, 185, 199, 208, and 212, indicating that
20 previously mapped sequences having similarity, but not complete identity, to SEQ ID NO:145, 152, 184, 185, 199, 208, and 212 were assembled into their respective clusters. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in
25 humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified
30 disease genes map within or in proximity to the intervals indicated above.

VI. Extension of TRFX Encoding Polynucleotides

The full length nucleic acid sequences of SEQ ID NO:108-214 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the

other primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was
5 quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

10 In like manner, the polynucleotide sequences of SEQ ID NO:108-214 are used to obtain 5' regulatory sequences using the procedure above, along with oligonucleotides designed for such extension, and an appropriate genomic library.

VII. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:108-214 are employed to screen cDNAs,
15 genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase
20 (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

25 The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and
30 compared.

VIII. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra),
mechanical microspotting technologies, and derivatives thereof. The substrate in each of the
35 aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999),

supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers.

Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40 μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37 °C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85 °C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μl 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5
5 µg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR
10 Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average
15 concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate
20 buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60 °C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample
25 mixture is heated to 65 °C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60 °C. The arrays are washed for 10 min at 45 °C in a first wash
30 buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45 °C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines

at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

IX. Complementary Polynucleotides

Sequences complementary to the TRFX-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring TRFX. Although use of

oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of TRFX. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the TRFX-encoding transcript.

X. Expression of TRFX

Expression and purification of TRFX is achieved using bacterial or virus-based expression systems. For expression of TRFX in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express TRFX upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of TRFX in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding TRFX by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, TRFX is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from TRFX at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995,

supra, ch. 10 and 16). Purified TRFX obtained by these methods can be used directly in the assays shown in Examples XI and XV.

XI. Demonstration of TRFX Activity

TRFX activity is measured by its ability to stimulate transcription of a reporter gene (Liu, H.Y. et al. (1997) EMBO J. 16(17):5289-5298). The assay entails the use of a well characterized reporter gene construct, LexA_{op}-LacZ, that consists of LexA DNA transcriptional control elements (LexA_{op}) fused to sequences encoding the *E. coli* LacZ enzyme. The methods for constructing and expressing fusion genes, introducing them into cells, and measuring LacZ enzyme activity, are well known to those skilled in the art. Sequences encoding TRFX are cloned into a plasmid that directs the synthesis of a fusion protein, LexA-TRFX, consisting of TRFX and a DNA binding domain derived from the LexA transcription factor. The resulting plasmid, encoding a LexA-TRFX fusion protein, is introduced into yeast cells along with a plasmid containing the LexA_{op}-LacZ reporter gene. The amount of LacZ enzyme activity associated with LexA-TRFX transfected cells, relative to control cells, is proportional to the amount of transcription stimulated by the TRFX.

XII. Functional Assays

TRFX function is assessed by expressing the sequences encoding TRFX at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT plasmid (Life Technologies) and pCR3.1 plasmid (Invitrogen), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are

discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of TRFX on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding TRFX and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding TRFX and other genes of interest can be analyzed by northern analysis or microarray techniques.

10 **XIII. Production of TRFX Specific Antibodies**

TRFX substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the TRFX amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using FMOC chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-TRFX activity by, for example, binding the peptide or TRFX to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIV. Purification of Naturally Occurring TRFX Using Specific Antibodies

Naturally occurring or recombinant TRFX is substantially purified by immunoaffinity chromatography using antibodies specific for TRFX. An immunoaffinity column is constructed by covalently coupling anti-TRFX antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing TRFX are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TRFX (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt

antibody/TRFX binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and TRFX is collected.

XV. Identification of Molecules Which Interact with TRFX

TRFX, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent.

- 5 (See, e.g., Bolton A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled TRFX, washed, and any wells with labeled TRFX complex are assayed. Data obtained using different concentrations of TRFX are used to calculate values for the number, affinity, and association of TRFX with the candidate molecules.

- 10 Alternatively, molecules interacting with TRFX are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989, Nature 340:245-246), or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

- TRFX may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions
15 between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

- Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the
20 invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	108	095210	PITUNOT01	095210H1 (PITUNOT01), 095210R1 (PITUNOT01), 450088R1 (TLYMNOT02), 1405954F6 (LATRTUT02), 1676067F6 (BLADNOT05), 3421076H1 (UCMCNOT04), 3519949H1 (LUNGNOT03), 3535670H1 (KIDNNOT25)
2	109	157953	THP1PLB02	157953F1 (THP1PLB02), 157953H1 (THP1PLB02), 2799335H1 (LIVRNOT02), 293820X24 (LIVRNOT04), 1210577R7 (BRSTNOT02), 2563416H1 (ADRETUT01), 5049562H1 (BRSTNOT33), 9678942
3	110	159196	ADENINB01	159196H1 (ADENINB01), 873479R1 (LUNGAST01), 1695224F6 (COLNNOT23), 4408025F6 (PROSDIT01), 4663865T6 (MEGBUNT01)
4	111	343338	THYMNOT02	343338H1 (THYMNOT02), 343338R6 (THYMNOT02), 343338T6 (THYMNOT02), 1448112F6 (PLACNOT02), 1448112R1 (PLACNOT02), 2235177X14F1 (PANCUTUT02), 2235177X16F1 (PANCUTUT02), 2235177X17F1 (PANCUTUT02), 2241778F6 (PANCUTUT02), 2241778T6 (PANCUTUT02), 2729457F6 (OVARUTUT05), 4053846F6 (SPLNNOT13), SBGA04252F1
5	112	402386	TMLR3DT01	402386H1 (TMLR3DT01), 402386X11 (TMLR3DT01), 568243R1 (MMLR3DT01), 568243T6 (MMLR3DT01), 731436H1 (LUNGNOT03), SAGA00508R1, SAGA00557R1
6	113	456487	KERANOT01	168091H1 (LIVRNOT01), 456487H1 (KERANOT01), 532096R1 (BRAINOT03), 619791H1 (PGANNOT01), 825933R1 (PROSNOT06), 1436382F1 (PANCNOT08), 1439054F6 (PANCNOT08), 1700156F6 (BLADTUT05), 2274307R6 (PROSNON01), 2515549H1 (LIVRTUT04), 5158675H1 (BRSTTMT02)
7	114	490256	HNT2AGT01	490256H1 (HNT2AGT01), 507309F1 (TMLR3DT02), 507309X15 (TMLR3DT02); 2724951H1 (OVARUTUT05), SZZZ00188R1, SZZZ02099R1, 9825070, 91242173
8	115	494740	HNT2NOT01	494740H1 (HNT2NOT01), 770196R1 (COLNCR01), 1235126F1 (LUNGFET03), 1235126T1 (LUNGFET03), 1326711F1 (LPARNOT02), 1816820F6 (PROSNOT20), 1853059H1 (LUNGFET03)
9	116	507475	TMLR3DT02	507475H1 (TMLR3DT02), 5359332R6 (ADRENOT03), 779955H1 (MYOMNOT01), 1928396T6 (BRSTNOT02), 2078558H1 (ISLTNOT01)
10	117	531581	BRAINOT03	084009X13 (HYPONOB01), 413713R1 (BRSTNOT01), 413718X22F1 (BRSTNOT01), 531581H1 (BRAINOT03), 531581T6 (BRAINOT03), 2171348H1 (ENDCNOT03), 2795710T6 (NPOLNOT01), 2926562F7 (TLYMNOT04), 2926562T7 (TLYMNOT04), 4341890H1 (BRAUNOT02), 4405904H1 (PROSDIT01)
11	118	675190	CRBLNOT01	675190H1 (CRBLNOT01), 675190X13 (CRBLNOT01), 1812672F6 (PROSTUT12), 2573205R6 (HIPOAZT01)
12	119	685434	UTRSNOT02	685434CT1 (UTRSNOT02), 685434H1 (UTRSNOT02), 1904155F6 (OVARNOT07), 2784031F6 (BRSTNOT13), 3129338F6 (LUNGUTUT12)

Table 1 (cont.)

Polyptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
13	120	788663	PROSNOT05	788663H1 (PROSNOT05), 1451931F1 (PENITUT01), 1960289H1 (BRSTNOT04), 2083142F6 (UTRSNOT08), 2542122H1 (BONRTUT01), 2581153F6 (KIDNTUT13), 3577780H1 (BRONNOT01)
14	121	870100	LUNGAST01	625091R6 (PGANNOT01), 870100H1 (LUNGAST01), 870100X12 (LUNGAST01), 1231358H1 (BRAITUT01), STEQ00206R1, SZZZ00601R1, SZZZ02045R1
15	122	879500	THYRNUT02	281880H1 (CARDNOT01), 859233R1 (BRAITUT03), 879500H1 (THYRNUT02), 1250675F6 (LUNGFET03), 1601165F6 (BLADNOT03), 1823981F6 (GBLATUT01), 2187360F6 (PROSNOT26), 2262956H1 (UTRSNOT02), 2433567H1 (BRAVUNT02), 2656846F6 (LUNGTUT09), 2993077F6 (KIDNFET02), 3085846H1 (HEAONOT03), 3181794T6 (TLYJNOT01), 4285141F6 (LIVRDIR01), 4774779H1 (BRAQNOT01), 5507484H1 (BRADDIR01), 5512965H1 (BRADDIR01), SCMA05658V1, SCMA03540V1, SCMA00007V1, g2224558
16	123	975377	MUSCNOT02	026851R1 (SPLNFET01), 786313R1 (PROSNOT05), 975377H1 (MUSCNOT02), 975377X19 (MUSCNOT02), 975377X21 (MUSCNOT02), 1354139X14 (LUNGNOT09), 2546208H1 (UTRSNOT11)
17	124	1208721	BRSTNOT02	1208721H1 (BRSTNOT02), 1286769F1 (BRAINOT11), 1456447F6 (COLNFET02), 1722840T6 (BLADNOT06), 1998475R6 (BRSTTUT03), 2740916F6 (BRSTTUT14), 3234886H1 (COLNUCT03), 4588959H1 (MASTTUT01), 4710080H1 (BRAIFET02), g1425135
18	125	1234329	LUNGFET03	259818T6 (HNT2RAT01), 264365H1 (HNT2AGT01), 349606H1 (LVENNOT01), 399059H1 (PITUNOT02), 1234329H1 (LUNGFET03), 1257012F1 (MENITUT03), 1442838F1 (THYRNUT03), 1443014R1 (THYRNUT03), 1515850F1 (PANCTUT01), 2186886F6 (PROSNOT26), 2655641F6 (THYMNUT04), 2703809F6 (OVARUTUT10), g1688736, g1985577
19	126	1238747	LUNGTUT02	501158R6 (NEUTLPT01), 565047H1 (NEUTLPT01), 769541R6 (COLNCR01), 890561T6 (STOMTUT01), 1238747H1 (LUNGTUT02), 1510233F6 (LUNGNOT14), 1510233T6 (LUNGNOT14)
20	127	1265980	BRAINOT09	1265980H1 (BRAINOT09), 2155287X13F1 (BRAINOT09), 2155287X23F1 (BRAINOT09), 2158376T6 (BRAINOT09), SAGA02430F1
21	128	1297333	BRSTNOT07	1297333H1 (BRSTNOT07), 1297333X12 (BRSTNOT07), 1297333X14 (BRSTNOT07), SAGA00259F1, SAGA00400R1

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
22	129	1312824	BLADTUT02	306400R6 (HEARNOT01), 1312824H1 (BLADTUT02), 1312824T6 (BLADTUT02), 1840110H1 (EOSITXT01), 1846489R6 (COLNNOT09), 1985201R6 (LUNGAST01), 2199162H1 (SPLNFET02), 2779784H1 (OVARFUT03), 3528903H1 (BLADNOT09), 3767951H1 (BRSTNOT24), 4251647H1 (BRADDIR01), 5205078H2 (BRAFNOT02), 5423679H1 (PROSTMT07), SANA02095F1, g1941058
23	130	1359294	LUNGNOT12	139446H1 (LIVRNOT01), 258759H1 (HNT2RAT01), 268845H1 (HNT2NOT01), 492813R1 (HNT2NOT01), 1213691H1 (BRSTTUT01), 1222480H1 (COLNUT02), 1243093H1 (LUNGNOT03), 1319296H1 (BLADNOT04), 1359294H1 (LUNGNOT12), 1404752F6 (LATRTUT02), 1404752T6 (LATRTUT02), 1479678H1 (CORPNOT02), 1558471H1 (SPLNNOT04), 1857126H1 (PROSNOT18), 1870761H1 (SKINBIT01)
24	131	1377380	LUNGNOT10	962085R1 (BRSTTUT03), 1377380H1 (LUNGNOT10), 1670530F6 (BMARNOT03), 1853551T6 (LUNGFET03), 2119555R6 (BRSTTUT02), SCIA03178V1
25	132	1383473	BRAITUT08	780421H1 (MYOMNOT01), 1344946F6 (PROSNOT11), 1383473F6 (BRAITUT08), 1383473H1 (BRAITUT08), 1906164T6 (OVARNOT07), 2302122R6 (BRSTNOT05), 2328233R6 (COLNNOT11), 2615335F6 (GBLANOT01), 5836742H1 (BRAIDIT05)
26	133	1388860	EOSINOT01	415763R1 (BRSTNOT01), 1388860H1 (EOSINOT01), SAFC02379F1, SAFC01030F1, SAFC00771F1, SAFC02719F1
27	134	1395322	THYRNOT03	1332909F6 (PANCNOT07), 1332909X16 (PANCNOT07), 1332909X23R1 (PANCNOT07), 1332909X24R1 (PANCNOT07), 1395322H1 (THYRNOT03), 1477406F1 (CORPNOT02), 3422017H1 (UCMCNOT04)
28	135	1419370	KIDNNOT09	243596H1 (HIPONOT01), 929439R1 (CERVNOT01), 1310519F1 (COLNFET02), 1395856T1 (THYRNOT03), 1419370F1 (KIDNNOT09), 1419370H1 (KIDNNOT09), 1666159F6 (BRSTNOT09), 3461531H1 (293TF2T01), 4710948H1 (BRAIFET02), SBGA01870F1, g947108, g1991693
29	136	1429773	SINTBST01	1306171T6 (PLACNOT02), 1313558F1 (BLADTUT02), 1429773H1 (SINTBST01), 1469411F1 (PANCUTUT02), 1626615F6 (COLNPOT01), 1807088F6 (SINTNOT13), 2641613F6 (LUNGTUT08), 2692245F6 (LUNGNOT23), 2695323H1 (UTRSNOT12), 2851378H1 (BRSTTUT13), 3387328F6 (LUNGTUT17)
30	137	1470820	PANCUTUT02	1232690F6 (LUNGFET03), 1470820H1 (PANCUTUT02), 1484705F1 (CORPNOT02), 2831707F6 (TLYMNOT03), 3073715H1 (BONEUNT01)
31	138	1483455	CORPNOT02	487811X26 (HNT2AGT01), 1483455H1 (CORPNOT02), 1849167F6 (LUNGFET03), 1856220F6 (PROSNOT18), 2822949F6 (ADRETUT06), 2822949T6 (ADRETUT06), 2851743F6 (BRSTTUT13), g2159610

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
32	139	1527064	UCMCL5T01	001612H1 (U937NOT01), 001923H1 (U937NOT01), 1235664H1 (LUNGFET03), 1412779H1 (BRAINOT12), 1527064H1 (UCMCL5T01), 1598233T6 (BLADNOT03), 1702565H1 (BLADTUT05), 1973691H1 (UCMCL5T01), 2227436H1 (SEMVNOT01), 2472092F6 (THP1NOT03), 2634126H1 (COLNTUT15)
33	140	1557491	BLADTUT04	046771H1 (CORNNOT01), 1456684F6 (COLNFET02), 1456684T6 (COLNFET02), 1554967F1 (BLADTUT04), 1557491H1 (BLADTUT04), 1992143H1 (CORPNOT02), 2687476F6 (LUNGNOT23), 3139175F6 (SMCCNOT02), 4746319H1 (SMCRUNT01)
34	141	1576862	LNODNOT03	496787F1 (HNT2NOT01), 496787R1 (HNT2NOT01), 1572855F6 (LNODNOT03), 1576862H1 (LNODNOT03), 1576862X11 (LNODNOT03), 1576862X19 (LNODNOT03), 1576862X21 (LNODNOT03), 3284579T6 (HEAONOT05), SBIA03851D1, SBIA04892D1, SBIA07089D1
35	142	1609731	COLNTUT06	112132F1 (PITUNOT01), 112132R1 (PITUNOT01), 159643X1 (ADENINB01), 1609731H1 (COLNTUT06), 1609731T6 (COLNTUT06), 5445363H1 (LNODNOT12), g2204797
36	143	1674538	BLADNOT05	1432420H1 (BEPINON01), 1579333F6 (DUODNOT01), 1674538F6 (BLADNOT05), 1674538H1 (BLADNOT05), 2656555H1 (LUNGTUT09), 4249348H1 (BRADDIR01), 4618275H1 (BRAYDIT01), 4760417H1 (BRAMNOT01), g3785154, g1623216, g899854, g1717534
37	144	1675287	BLADNOT05	868686T1 (LUNGAST01), 984876R1 (LVENNOT03), 1456253F1 (COLNFET02), 1675287H1 (BLADNOT05), 1675845H1 (BLADNOT05), 2047281F6 (THP1T7T01), 2808537H1 (BLADTUT08), 4883514F6 (LUNLTUT01)
38	145	1693903	COLNNOT23	1358877F1 (LUNGNOT09), 1573956F1 (LNODNOT03), 1693903F6 (COLNNOT23), 1693903H1 (COLNNOT23), 2184065F6 (SININOT01), 3316112F6 (PROSBPT03), SXAF02294V1
39	146	1702962	DUODNOT02	794279R6 (OVARNOT03), 814285R6 (OVARNOT03), 1702962H1 (DUODNOT02), 2186132H1 (PROSNOT26), 2880019F6 (UTRSTUT05), 5196364H1 (LUNLTUT04)
40	147	1712916	PROSNOT16	1712916F6 (PROSNOT16), 1712916H1 (PROSNOT16), 2186575F6 (PROSNOT26), g3399946
41	148	1748313	STOMTUT02	940469R6 (ADRENOT03), 1317481F6 (BLADTUT02), 1748313H1 (STOMTUT02), 1870549F6 (SKINBIT01), 2169544F6 (ENDCNOT03), 2285816H1 (BRAINON01), 2383066F6 (ISLTNOT01), 2613757F6 (ESOGTUT02), SZAS01459V1, SZAS00220V1
42	149	1754833	LIVRTUT01	710767H1 (SYNORAT04), 1396892F6 (BRAITUT08), 1754833H1 (LIVRTUT01), 1754833T6 (LIVRTUT01), 1879592F6 (LEURNOT03), 2331424R6 (COLNNOT11), 3125146H1 (LNODNOT05), 3212201H1 (BLADNOT08), 3585117H1 (293TF4T01)

Table 1 (cont.)

Polyptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
43	150	1798701	COLNNOT27	122777F1 (LUNGNOT01), 122777R1 (LUNGNOT01), 1215026R6 (BRSTTUT01), 1753224H1 (LIVRTUT01), 1798701H1 (COLNNOT27), 2041087H1 (HIPONON02), SAEA00596F1, SAEA00135F1
44	151	1842496	COLNNOT07	027249F1 (SPLNFET01), 1330406H1 (PANCNOT07), 1842496H1 (COLNNOT07), 1981256R6 (LUNGNOT03), 3215321F7 (TESTNOT07)
45	152	1868613	SKINBIT01	1868613H1 (SKINBIT01), 1999115R6 (BRSTTUT03), 2159835F7 (ENDCNOT02), 2453392H1 (ENDANOT01), 2753832H1 (THPLAZS08), 2781021T6 (OVARUT03), 3597161F6 (FIBPNOT01), 4567678H1 (HELATXT01), 4998328H1 (MYEPTXT02)
46	153	1870609	SKINBIT01	474617H1 (MMLR1DT01), 1391829F6 (THYRNOT03), 1722968F6 (BLADNOT06), 1722968T6 (BLADNOT06), 1833131H1 (BRAINON01), 1870609F6 (SKINBIT01), 1870609H1 (SKINBIT01), 1870609T6 (SKINBIT01), 2542675H2 (UTRSNOT11), 2580351F6 (KIDNTUT13), 2653740H1 (THYMNOT04), 3228774H1 (COTRNOT01)
47	154	1871961	LEUKNOT02	743684F1 (BRAITUT01), 835705R1 (PROSNOT07), 1624519F6 (BRAITUT13), 1688618F6 (PROSTUT10), 1871961F6 (LEUKNOT02), 1871961H1 (LEUKNOT02), 1965802R6 (BRSTNOT04), 2453823F6 (ENDANOT01), 4689940H1 (PROSTMT05)
48	155	1876258	LEUKNOT02	808836R1 (LUNGNOT04), 1390870H1 (EOSINOT01), 1876258H1 (LEUKNOT02), SZAHO0430F1, SZAHO3995F1, SZAHO0534F1, SZAHO1526F1
49	156	1929822	COLNTUT03	040201F1 (TBLYNOT01), 424589R6 (BLADNOT01), 638245H1 (BRSTNOT03), 1251025F1 (LUNGFET03), 1391470H1 (EOSINOT01), 1699355F6 (BLADTUT05), 1929822H1 (COLNTUT03), 2218644H1 (LUNGNOT18), 2291751R6 (BRAINON01), 3242060H1 (COLAUCT01), 3317796F6 (PROSBPT03), 3401711H1 (ESOGNOT03), 3488355H1 (EPIGNOT01), 4030773H1 (BRAINOT23), 4180362H1 (SINITUT03), 4891448H1 (PROSTMT05), 5539034H1 (KIDNFEC01), 93882288
50	157	1970095	UCMCL5T01	114097F1 (TESTNOT01), 168757H1 (LIVRNOT01), 754038R1 (BRAITUT02), 772953R1 (COLNCRT01), 880261R1 (THYRNOT02), 1970095F6 (UCMCL5T01), 1970095H1 (UCMCL5T01), 2235148F6 (PANCUTUT02), SAEA02374R1
51	158	1975473	PANCUTUT02	1340447F1 (COLNTUT03), 1500133F6 (SINTBST01), 1663908F6 (BRSTNOT09), 1975473H1 (PANCUTUT02), 3726008H1 (BRSTNOT23)
52	159	1976527	PANCUTUT02	160328R6 (ADENINB01), 982222T2 (TONGTUT01), 993118R6 (COLNNOT11), 1709642T6 (PROSNOT16), 1976527F6 (PANCUTUT02), 1976527H1 (PANCUTUT02), 3586151F6 (293TF4T01), SXAE03918V1, SXAE05371V1
53	160	2108023	BRAITUT03	1493429H1 (PROSNON01), 2012466H1 (TESTNOT03), 2108023H1 (BRAITUT03), 2108023T6 (BRAITUT03)

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
54	161	2135746	ENDCNOT01	998857R6 (KIDNTUT01), 1384325F1 (BRAITUT08), 1727569F6 (PROSNOT14), 2135746F6 (ENDCNOT01), 2135746H1 (ENDCNOT01), 2255539R6 (OVRTUT01), 2999008H1 (OVRTUT07), 3623266H1 (ENDANOT03), 5412531H1 (BRATNOT03)
55	162	2154810	BRAINOT09	035033X11 (HUVENOB01), 035033X14 (HUVENOB01), 1857664F6 (PROSNOT18), 1857664T6 (PROSNOT18), 2154810H1 (BRAINOT09), 2847166T6 (DRGLNOT01), 5094009F6 (EPIMN05)
56	163	2228991	PROSNOT16	2228991F6 (PROSNOT16), 2228991H1 (PROSNOT16), 3970066F6 (PROSTUT10)
57	164	2241206	PANCUTUT02	1235632F6 (LUNGFT03), 1514392F1 (PANCUTUT01), 1533915F1 (SPLNNOT04), 2241206H1 (PANCUTUT02), 2724267X303D1 (LUNGUTUT10), 5218584T6 (BRSTNOT35), 5567773H1 (TLYMN08)
58	165	2259590	OVRTUT01	935085T1 (CERVNOT01), 1915979H1 (PROSTUT04), 2259590H1 (OVRTUT01), 2259590R6 (OVRTUT01), 2259590T6 (OVRTUT01)
59	166	2307537	NGANNOT01	628086T6 (KIDNNOT05), 931221T6 (CERVNOT01), 2307537H1 (NGANNOT01), 2307537R6 (NGANNOT01), 2799812H1 (PENCNOT01), 3318983H1 (PROSBPT03), 4158531F6 (ADRENOT14), SBZA00461V1, SBZA04079V1
60	167	2440675	EOSITXT01	806660R6 (BSTNNOT01), 1390870H1 (EOSINOT01), 2440675H1 (EOSITXT01), SZAH00430F1, SZAH03995F1, SZAH00534F1, SZAH01526F1
61	168	2463542	THYRNOT08	2463542F6 (THYRNOT08), 2463542H1 (THYRNOT08), 2552885F6 (THYMNOT03), 2655535F7 (THYMNOT04), 2869957T6 (THYRNOT10), 3042074F7 (BRSTNOT16), 3769037H1 (BRSTNOT24), 3801333H1 (SPLNNOT12), 3927329H1 (KIDNNOT19)
62	169	2486031	CONUTUT01	1417222F6 (BRAINOT12), 2486031F6 (CONUTUT01), 2486031H1 (CONUTUT01), 2634120X315D2 (COLNTUT15), 2951631T6 (KIDNFET01), 93806506
63	170	2493052	ADRETUT05	1376888F6 (LUNGNOT10), 148851F6 (UCMCL5T01), 2108437R6 (BRAITUT03), 2493052F7 (ADRETUT05), 2493052H1 (ADRETUT05), 2493052T6 (ADRETUT05), 2840241F6 (DRGLNOT01), 4364312H1 (SKIRNOT01)
64	171	2512074	CONUTUT01	008250X12 (HMCINOT01), 030534X12 (THPINOB01), 1686214F6 (PROSNOT15), 2395458F6 (THPIAZT01), 2512074H1 (CONUTUT01), 2963912F6 (SCORNOT04), 5326933F6 (DRGTN04)
65	172	2646274	LUNGUTUT11	724811R6 (SYNOAT01), 2646274H1 (LUNGUTUT11), 3436027F6 (PENCNOT05)
66	173	2672566	KIDNNOT19	1381053F1 (BRAITUT08), 2108293R6 (BRAITUT03), 2672566H1 (KIDNNOT19), 2908546F6 (THYMNOT05), 3730092H1 (SMCCN03)
67	174	2689674	LUNGNOT23	2256960T6 (OVRTUT01), 2507571F6 (CONUTUT01), 2689674F6 (LUNGNOT23), 2689674H1 (LUNGNOT23), 2755742H1 (THPIAZS08), 5096438H1 (EPIMN05)

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
68	175	2703282	OVARTUT10	056400H1 (FIBRNOT01), 1484887F6 (CORPNOT02), 1484887T6 (CORPNOT02), 1641813F6 (HEARFET01), 1810188H1 (PROSTUT12), 2351291F6 (COLSUCT01), 2703282H1 (OVARTUT10), 3790456H1 (BRSTNOT28), 4084543T6 (CONFNOT02), 4994160H1 (LIVRTUT11), 5393763H1 (KIDNNOT32)
69	176	2738293	OVARNOT09	412176R1 (BRSTNOT01), 418633T6 (BRSTNOT01), 12322594F1 (LUNGFET03), 1301651T6 (BRSTNOT07), 2738293F6 (OVARNOT09), 2738293H1 (OVARNOT09), 5290883H1 (LIVRTUS02)
70	177	2772776	PANCNOT15	784334R1 (PROSNOT05), 2772776H1 (PANCNOT15), 3750404H1 (UTRSNOT18)
71	178	2774476	PANCNOT15	2774476H1 (PANCNOT15), 3664676T6 (PANCNOT16), 3835889F6 (PANCNOT17), 4167883X305V1 (PANCNOT21), SCCA02152V1
72	179	2804624	BLADTUT08	162435R1 (ADENINB01), 1304830T1 (PLACNOT02), 2080378X19F1 (UTRSNOT08), 2660596H1 (LUNGUT09), 2804624H1 (BLADTUT08)
73	180	2848225	BRSTTUT13	346073X101 (THYMNOT02), 346073X26C1 (THYMNOT02), 391609T6 (TMLR2DT01), 2848225H1 (BRSTTUT13), 4624612T6 (ENDVNOT01)
74	181	2882241	UTRSTUT05	1637060F6 (UTRSNOT06), 1711682F6 (PROSNOT16), 1902475H1 (OVARNOT07), 2017387F6 (THP1NOT01), 2882241F6 (UTRSTUT05), 2882241H1 (UTRSTUT05), 3532864H1 (KIDNNOT25)
75	182	2939011	THYMFET02	897237R1 (BRSTNOT05), 897237T1 (BRSTNOT05), 1618381F6 (BRAITUT12), 2679105F6 (SINIUCT01), 2939011F6 (THYMFET02), 2939011H1 (THYMFET02), 2939011T6 (THYMFET02)
76	183	2947188	BRAITUT23	377292X1 (NEUTFMT01), 425953R6 (BLADNOT01), 425953T6 (BLADNOT01), 425953X28 (BLADNOT01), 429350T6 (BLADNOT01), 451192F1 (TLYMNOT02), 451192R1 (TLYMNOT02), 1786579H1 (BRAINOT10), 2947188H1 (BRAITUT23)
77	184	3094001	BRSTNOT19	1494663T6 (PROSNOT01), 2083139X11F1 (UTRSNOT08), 3094001H1 (BRSTNOT19)
78	185	3110061	BRSTTUT15	986428R6 (LVENNOT03), 1449222R1 (PLACNOT02), 3085841F6 (HEAONOT03), 3110061F7 (BRSTTUT15), 3110061H1 (BRSTTUT15), 4308349T6 (BRAUNOT01), 4637040F6 (MYEPTXT01)
79	186	3146614	PENCNOT06	638370R1 (BRSTNOT03), 1398786T1 (BRAITUT08), 1435622F1 (PANCNOT08), 1720684F6 (BLADNOT06), 2194122F6 (THYRTUT03), 2459594H1 (THYRNOT08), 3146614H1 (PENCNOT06), 3278069H1 (STOMFET02), 3357696F6 (PROSTUT16)
80	187	3295381	TLYJINT01	2222227F6 (LUNGNOT18), 3295381H1 (TLYJINT01), SZZZ00995R1, SZZZ00226R1, SZZZ00209R1, SZZZ00347R1, SZZZ00451R1

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
81	188	3364774	PROSBT02	1339847F6 (COLNTUT03), 1415866F6 (BRAINT012), 2458556T6 (ENDANOT01), 2515467F6 (LIVRTUT04), 2523246H1 (BRAITUT21), 3095773H1 (CERVNOT03), 3315208F6 (293TF2T01), 3364774H1 (PROSBT02), 3697590H1 (SININOT05), 4618612H1 (BRAYDIT01), 91422476
82	189	3397777	UTRSNOT16	2906192F6 (THYMNOT05), 3046506F7 (HEAANOT01), 3045506X329D1 (HEAANOT01), 3046506X331D1 (HEAANOT01), 3397777F7 (UTRSNOT16), 3397777H1 (UTRSNOT16), 3846636H1 (DENDNOT01), 4569754H2 (PROSTUT21)
83	190	3403046	ESOGNOT03	2754425R6 (THPLAZS08), 3403046H1 (ESOGNOT03), 3844619F6 (DENDNOT01)
84	191	3538506	SEMVNOT04	483831H1 (HNT2RAT01), 1451166F1 (PENITUT01), 3187785H1 (THYMNON04), 3538506F6 (SEMVNOT04), 3538506H1 (SEMVNOT04), 3868721F6 (BMARNOT03), 5108547F6 (PROSTUS19), 5163595H1 (ENDIUNT01), 5324664H1 (FIBPFEN06), 92056736
85	192	3575519	BRONNOT01	970343R6 (MUSCNOT02), 975169R6 (MUSCNOT02), 3575519H1 (BRONNOT01), SCSA04735V1, SCSA03846V1
86	193	3598694	FIBPNOT01	1330295P1 (PANCNOT07), 3332508T6 (BRAIFET01), 3520552H1 (LUNGNON03), 3598694H1 (FIBPNOT01), 5203510H1 (STOMNOT08), 5506937H1 (BRADDIR01), SCCA00526V1, SCCA04468V1, SCCA03065V1, SCCA02377V1, SCCA00888V1, SCCA02832V1
87	194	3638819	LUNGNOT30	837827X22 (PROSNOT07), 837827X23 (PROSNOT07), 3638819H1 (LUNGNOT30)
88	195	3717139	PENCNOT10	3717139H1 (PENCNOT10), g2106014, g2980871
89	196	3892962	BRSTTUT16	594617R6 (BRAVUNT02), 837890X18 (PROSNOT07), 1961640R6 (BRSTNOT04), 2330093H1 (COLNNOT11), 2726737F6 (OVARNTUT05), 3892962H1 (BRSTTUT16)
90	197	4153521	MUSLTMT01	118141F1 (MUSCNOT01), 487811X24 (HNT2AGT01), 487811X26 (HNT2AGT01), 868070R6 (BRAITUT03), 1832527T6 (BRAINON01), 2851743T6 (BRSTTUT13), 4153521H1 (MUSLTMT01), 4531734H1 (PROSTMT03), SZZZ01004R1
91	198	4585038	OVARNOT13	546958R6 (BEPINOT01), 656154H1 (EOSINOT03), 3415219H1 (PTHYNOT04), 3683524H1 (HEAANOT01), 3750253H1 (UTRSNOT18), 4089875H1 (LIVRNOT06), 4585038H1 (OVARNT013), g756767, g756768
92	199	4674640	NOSEDIT02	191268R1 (SYNORAB01), 1414304F6 (BRAINT012), 3272067F6 (BRAINT020), 4674640H1 (NOSEDIT02), SCDA05786V1, SCDA07745V1, SZAP01877V1
93	200	4676066	NOSEDIT02	875407R1 (LUNGAST01), 1478971F6 (CORPNOT02), 1749564F6 (STOMTUT02), 2263128H1 (UTRSNOT02), 4676066H1 (NOSEDIT02), 5449856H1 (BSCNDIT02), 5487675H1 (DRGTN04), g3118452
94	201	4830687	BRAVXT03	534025F1 (BRAINOT03), 4830687H1 (BRAVXT03)

Table 1 (cont.)

Polyptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
95	202	4880891	UTRWTMT01	055751H1 (FIBRN0T01), 1288342F6 (BRAIN0T11), 1288342T6 (BRAIN0T11), 1396095F6 (THYRN0T03), 1820602F6 (GBLAT0T01), 2123331F6 (BRSTN0T07), 2462011F6 (THYRN0T08), 2645165X303D1 (OVAR0T03), 2666343H1 (ADRET0T06), 2666343T6 (ADRET0T06), 2715208F6 (THYRN0T09), 2881019F6 (UTRST0T05), 3448078X331D1 (UTRSN0T3), 4880891H1 (UTRMT0T01), 5465061H1 (LNODN0T11), 5503746H1 (BRABDIR01), SBLA03155F1, SBLA02267F1
96	203	4909754	THYMDIT01	014580H1 (THP1PLB01), 1348640F6 (PROSN0T11), 1685157F6 (PROSN0T15), 3427741H1 (BRSTN0R01), 3540578H1 (SEMVN0T04), 4909754F6 (THYMDIT01), 4909754H1 (THYMDIT01), 5834707H1 (BRAIDIT05), g1940399
97	204	4911931	THYMDIT01	428504F1 (BLADN0T01), 468041R6 (LATRN0T01), 2342984F6 (TESTTUT02), 2887138H1 (SINJN0T02), 4911931H1 (THYMDIT01)
98	205	4920433	TESTN0T11	2006765R6 (TESTN0T03), 4920433F6 (TESTN0T11), 4920433H1 (TESTN0T11)
99	206	5042113	COLHTTUT01	537782R6 (LNODN0T02), 537782T6 (LNODN0T02), 724003H1 (SYNOOAT01), 2700935X302B2 (OVAR0T03), 2700935X302F1 (OVAR0T03), 3572973T6 (BRONN0T01), 5042113H1 (COLHTTUT01), SBLA02608D1, SBLA08390D1
100	207	5083853	LN0GTUT01	1537455H1 (SINTTUT01), 5083853F6 (LN0GTUT01), 5083853H1 (LN0GTUT01), 5083853T6 (LN0GTUT01)
101	208	5283981	TESTN0N04	542319F1 (OVARN0T02), 542319X15F1 (OVARN0T02), 542319X17F1 (OVARN0T02), 1710519F6 (PROSN0T16), 5283981H1 (TESTN0N04)
102	209	5510549	BRADDIR01	1257226F6 (MENITUT03), 1654887F6 (PROSTUT08), 1866033F6 (PROSN0T19), 2309180H1 (NGANN0T01), 2516285F6 (LIVRTUT04), 3558606H1 (LUNGNOT31), 4689374H1 (LIVRTUT11), 5510549H1 (BRADDIR01)
103	210	5544862	TESTNOC01	1210853R1 (BRSTN0T02), 1803417F6 (SINTN0T13), 5544862F6 (TESTNOC01), 5544862H1 (TESTNOC01), 5544862T6 (TESTNOC01), 5547247F6 (TESTNOC01), g989649, g3246546, g2112974, g697810
104	211	5573394	TYLYMNOT08	027981H1 (SPLNFET01), 310525T6 (TMLR2DT01), 826528R1 (PROSN0T06), 868061R6 (BRAITUT03), 1985188T6 (LUNGAST01), 2207165F6 (SINTFET03), 5507004H1 (BRADDIR01), 55733394H1 (TYLYMNOT08), SBLA11388D1, SBLA11986D1, SBLA03475D1
105	212	5850840	FIBAUNT02	232422F1 (SINTN0T02), 232442R1 (SINTN0T02), 826837R1 (PROSN0T06), 1286853F1 (BRAIN0T11), 2058494R6 (OVARN0T03), 2842471F6 (DRGLN0T01), 3105825F6 (BRSTTUT15), 3617707H1 (EPIPNOT01), 3620903H1 (BRSTN0T25), 4148432H1 (SINITUT04), 5850840H1 (FIBAUNT02)
106	213	5942936	COLADIT05	121785R6 (MUSCNOT01), 797379T6 (OVARN0T03), 797379X14R1 (OVARN0T03), 797379X25R1 (OVARN0T03), 3690756H1 (HEARN0T01), 5942936H1 (COLADIT05)

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
107	214	5951431	LIVRTUN04	623984R6 (PGANNOT01), 676513T6 (CRBLNOT01), 1730442F6 (BRSTTUT08), 2640175F6 (LUNGTTUT08), 3360767F6 (PROSTUT16), 5951431H1 (LIVRTUN04), SAEA03186R1

Table 2

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
1 095210	463	S72 T7 S16 S49 T371 T58 S68 S72	N38 N53	ATP/GTP-binding site motif A (P-loop): G412-S419 Zinc finger C2H2 type domain: C133-H153 C161-H181 C189-H209 C217-H237 C245-H265 C273-H293 C301-H321 C329-H349 C357-H377 C385-H405 C413-H423 C441-H461 KRAB box domain: V6- R66	g498721 zinc finger protein [Homo sapiens] Abrink, M. et al. (1995) DNA Cell Biol. 14:125-136	MOTIFS BLAST_GENBANK BLAST_PFBM BLIMPS_BLOCKS BLIMPS_PRODUM BLAST_DOMO
2 157953	216	T28 T140 T2 T139 S210	N152	bZIP transcription factors basic domain signature: K147-R163	g4996451 leucine- zipper protein	MOTIFS BLAST_GENBANK BLAST_PFBM BLIMPS_BLOCKS BLAST_DOMO
3 159196	284	S153 S44 T189 T232 S3 T62 S125 S148 T245 Y140 Y196	N94 N95 N207	Zinc finger C2H2 type domain: C86-H106 C114- H134 C142-H162 C170- H190 C198-H218 C226- H246 C254-H274	g55471 Zinc finger protein expressed in post-meiotic spermatogenesis Denny, P. and Ashworth, A. (1991) Gene 106:221-227	MOTIFS BLAST_GENBANK BLAST_PFBM

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
4	343338 1416	S817 T406 S142 S236 S272 S329 S395 S412 S413 T426 S427 S439 S474 S475 S476 T531 S669 S711 T735 T832 S876 S878 T954 T960 S972 S1051 T1138 S1378 T42 S141 T262 T307 S315 T336 T345 S381 T400 T469 S482 S506 T625 T634 T707 T803 S843 S869 S891 T892 S993 S1002 T1033 S1103 T31 S1143 S1169 T1317 S1329 S1336 S1397 Y658 T1406 Y346 Y813 Y945 Y970	N40 N261 N409 N467 N1040 N1130 N1167	ATP/GTP-binding site motif A (P-loop): A1086-T1093 A1131- T1138 Beta-transducin family Trp-Asp repeats signature: V34-S48 L77-L91 Bromodomain signature: A778-H853, P935-T991	g7717364 homolog to CAMP response element binding and beta transducin family proteins [Homo sapiens]	MOTIFS BLAST_GENBANK BLAST_PFBM PROFILESSCAN BLIMPS_PRINTS BLAST_PRODOM BLAST_DOMO
5	402386 426	S292 T14 S65 S115 S24 T36 T139 T164 T192 S196 S380 Y229	N12	Zinc finger C2H2 type domain: F6-G44, C102- H124, Y169-H191, C171- H191, Y225-H247, Y253- H276, H282-H304, Y310- H332, Y338-H360, Y366- H388 KRAB box domain: V4- V67	g487785 zinc finger protein ZNF136 Tommerup, N. and Vissing, H. (1995) Genomics 27:259-264	MOTIFS BLAST_GENBANK BLAST_PFBM BLIMPS-PRODOM BLAST_PRODOM BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
6	456487 686	S407 T408 S27 S94 S117 T176 S185 T224 S225 S260 S318 T426 T427 S460 S542 S558 T559 S569 T595 S611 T618 S668 T6 T135 S247 S256 S278 S293 T299 T337 S357 S386 S451 S555	N79 N128 N213 N616	Putative GTPase activating protein for Arf: A464-E584 HIV REV interacting protein: N476-R512, V516-N537 Zinc finger motif: Q468-P581	g3880859 similar to Ank repeat (2 domains)	MOTIFS BLAST_GENBANK BLAST_PFAM BLIMPS_PRINTS BLIMPS_PRODROM BLAST_DOMO
7	490256 348	T3 T108 T114 T163 T181 S29 S134 S302		Zinc finger C2H2 type domain: C238-H258 C266-H286 C294-H314 C322-H342 Zinc finger motif: E8- Q173	g2316003 zinc finger protein [Homo sapiens] Lee, P.L. et al. (1997) Genomics 43:191-201	MOTIFS BLAST_GENBANK BLAST_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODROM BLAST_DOMO
8	494740 181	T22 T37 S60 T78 T87 S12 T70 T124 S157		Zinc finger motif: F79-G117 KRAB box: V77-R126	g487836 transcription factor	MOTIFS BLAST_GENBANK BLAST_PFAM BLIMPS_PRODROM BLAST_PRODROM BLAST_DOMO
9	507475 126	S2 S15 S71 S104 Y97		TFIIS zinc ribbon domain signature: G65- K123	g7212805 transcription- associated zinc ribbon protein [Homo sapiens] Fan, W. et al. (2000) Genomics 63:139-141	MOTIFS BLAST_GENBANK PROFILES SCAN BLIMPS_BLOCKS BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
10 531581	610	S177 S410 T438 T466 S44 S55 S125 T146 S233 S239 S282 S289 S482 S507 S523 S531 S532 T537 S539 T179 S188 T255 S279 S316 S462 Y81 Y415 Y443 Y471	N194 N206	Zinc finger C2H2 type domain: C304-H324 C332-H352 C360-H381 C389-H409 C417-H437 C445-H465 C473-H493 C501-H522 Zinc finger activator domain: M9-E124	g8843908 zinc finger protein SBBIZ1 [Homo sapiens]	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODOR BLAST_PRODOR BLAST_DOMO
11 675190	111	T102 S17 S24 T33 T67 S9 S43 S97	N3	Zinc finger protein domain: F25-G63 KRAB box domain: S22- P94	g10442700 zinc-finger protein ZERK1 [Homo sapiens] Zheng L. et al. (2000) Mol Cell 6:757-768 g4336830 RFX-Bdelta4 immunodeficiency- associated transcription factor Nagarajan, U.M. et al. (1999) Immunity 10:153-162	MOTIFS BLAST_GENBANK BLIMPS_PRODOR BLAST_DOMO BLAST_PFAM
12 685434	152	T6 T17 S109	N15		G2583171 CCAAT-binding transcription factor subunit AAB-1 Chen, H. et al. (1998) Genetics 148:123-130	MOTIFS BLAST_GENBANK BLAST_DOMO
13 788663	131	S30 S65 T73 S124 T45 S60 S65	N122	Transcription factor domain: R15-K96	gl89044 zinc finger protein 42 (MZF-1, preferentially expressed in myeloma cells) Hromas, R. et al. (1991) J Biol Chem 266:14183-14187	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODOR
14 870100	541	S7 S24 S69 S85 S99 S253 T255 T302 S505 S151 T245 T315 S356 S521	N192 N450 N454	Zinc finger C2H2 type domain: C152-H172, C180-H200, C208-H228, C362-H382, C390-H410, C418-H438, C446-H466, C474-H494		

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
15 879500	1828	S1194 S1283 S1307 S1390 S1395 S1467 S1530 S1554 S1614 S1629 S1651 S1652 S1653 S1717 S1766 S1770 S1775 S1820 S323 S443 S487 S497 S691 S716 S767 S822 S894 S921 S926 S980 S994 T1271 T1322 T1333 T1354 T1482 T1712 T1731 T1784 T322 T451 T549 T692 T727 T770 T803 T908 T976	N174 N725 N794 N1197	Helicases conserved c- terminal domain: D672- G755	g5104572 transcriptional activator SRCAP Johnston, H. et al. (1999) J Biol Chem 274:16370-16376	MOTIFS BLAST_GENBANK HMMER_Pfam BLAST_PRODOR BLAST_DOMO
16 975377	482	S185 S200 S258 S295 S319 S330 S366 S408 S463 T118 T123 T196 T205 T209 T461 T60 Y230 Y77	N306	Zinc finger C3HC4 type signature: K57-L112, I208-C236, C305-I314	g1304599 ZNF127-Xp (associated with Prader-Willi behavioral syndrome) Jong, M.T. et al. (1999) Hum Mol Genet 8:783-793	MOTIFS BLAST_GENBANK BLAST_Pfam BLIMPS_BLOCKS
17 1208721	264	S11 S59 T100 T114 T235 S259 S23 S138				MOTIFS
18 1234329	350	S170 S229 T290 S303 S129 S235 T331		Zinc finger C3HC4 type signature: C298-C338 PHD-finger: R313-Q327	g3880441 similar to zinc finger C3HC4 type	MOTIFS BLAST_GENBANK HMMER_Pfam PROFILES SCAN BLIMPS_Pfam

Table 2 (cont.)

Polypeptide SEQ ID NO.	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
19 1238747	549	S102 S175 S248 S273 S296 S303 S329 S346 S364 S437 S438 S485 T201 T271 T287 T370 T375 T396 T44 T467 T498 T524 T70	N77 N328	SAND DNA-binding domain: S454-L535	g9964115 transcriptional coactivator Sp110 [Homo sapiens] Bloch, D.B. et al. (2000) Mol Cell Biol 20:6138-6146	MOTIFS BLAST_GENBANK HMMER_PFAM
20 1265980	337	S22 T84 T85 T56 S131 S238 S242 T247 T326 S47 T56 T127 T135 S230 S272 Y281		Helix-loop-helix DNA binding domain: R95- S147, M1-L73 Myc-type 'helix-loop- helix' dimerization domain signature: E103-R118, T127-S147, N111-N164, E66-Q171 Transcription regulation domain: R191-N337	g4566748 basic helix- loop-helix transcription factor Ndr1 Liao, J. et al. (1999) DNA Cell Biol 18:333- 344	MOTIFS BLAST_GENBANK HMMER_PFAM PROFILES SCAN BLIMPS_BLOCKS BLAST_PRODROM BLAST_DOMO
21 1297333	581	S16 S29 T41 S47 T35 S92 S110 T184 S254 T368 S480 S493 S531 Y56 Y89	N78 N90 N201 N426	Zinc finger C2H2 type domain: C135-H155 C163-H183 C191-H212, C220-H240, C248-H268, C276-H296 C304-H324 C332-H352 C360-H380, C388-H408, C416-H436, C444-H464, C472-H492, C500-H520	g387079 zinc finger protein (mkr5) Chowdhury, K. et al. (1988) Nucleic Acids Res 16:9995-10011	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODROM BLAST_PRODROM BLAST_DOMO
22 1312824	591	S126 S127 S167 S278 S293 S389 S404 S435 S460 S510 S546 S64 S88 T203 T298 T377 T554 Y233	N296 N384 N489	Ets-related transcription factor domain: D273-P591, I180-F261 I180-K193, E206-K224, H225-Y243, Y244-K262	g972940 Elf-1 Transcription regulation protein Davis, J.N. and Roussel, M.F. (1996) Gene 171:265-269	MOTIFS BLAST_GENBANK HMMER_PFAM PROFILES SCAN BLIMPS_BLOCKS BLIMPS_PRINTS BLAST_PRODROM BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
23 1359294	767	S141 S391 S43 S461 S463 S485 S567 S620 S664 S75 T111 T201 T278 T291 T301 T494 T580 T646 T696 T730 T79	N18 N288 N549 N728	'Cold-shock' DNA- binding domain signature: Y37-V88, L121-M146, F166-R215 F329-V365, F499-N549, F654-W705 Unr protein DNA binding repeat domain: E98-D767	g57455 unr protein Ferrer, N. et al. (1999) DNA Cell Biol 18:209-218	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLAST_PRODUM BLAST_DOMO
24 1377380	206	S11 S131 S15 S152 S163 S167 S181 S193 S2 S34 S38 S84 S85 S93 T51			g7012714 L2DTL WD-40 repeat protein [Homo sapiens]	MOTIFS BLAST_GENBANK
25 1383473	352	S74 T95 T154 S165 S222 S322 S207 S236 S297 S308	N104 N205	Signal peptide motif: M1-A23 Transmembrane motif: L243-L259, C302-C339 Baculovirus inhibitor of apoptosis protein repeat (BIR): L298- C336	g4587558 Similar to X- linked apoptosis inhibitor	MOTIFS BLAST_GENBANK HMMER
26 1388860	532	S153 S27 S409 S465 S520 T103 T17 T360 T39 T49 Y138 Y367	N42 N65	Zinc finger C2H2 type domain: C201-H221 C229-H249 C257-H277 C285-H305 C313-H333 C341-H361 C369-H389 C397-H417 C425-H445, C453-H473, C481-H500, C508-H528 Zinc finger domain: F9-G47, K48-K146 KRAB box domain: D5- E78	g4519270 Kruppel-type zinc finger protein Kato, O. (1998) Biochem. Biophys. Res. Commun. 249:595-600	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM BLAST_PRODUM BLAST_DOMO
27 1395322	444	S105 S134 S155 S319 S375 T110 T291 T347 T378 T69 T7 T88 Y40	N54 N153 N166 N287	Zinc finger C2H2 type domain: C283-H303, C311-H331, C339-H359 C367-H387 C420-H440	g6063139 POZ/zinc finger transcription factor ODA-8 [Mus musculus]	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
28 1419370	347	S183 T307 T14 T263 T300		Zinc finger C3HC4 type signature: C164-C202	g11611473 Deltex3 Kishi, N. et al. (2001) Int. J. Dev. Neurosci. 19:21-35	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS PROFILES SCAN
29 1429773	308	S29 S31 T250 S257 Y130	N112	Transmembrane domain: P213-M237	g7542723 DHHC1 protein [Homo sapiens]	MOTIFS BLAST_GENBANK HMMER
30 1470820	80	S14 S32 T21 S36 S72 Y63		GC-rich sequence DNA binding factor domain: R11-V75 (P-value = 5.9 x 10 ⁻⁶)		MOTIFS
31 1483455	570	S116 S132 S181 S211 S470 S564 S70 S79 S87 T14 T143 T168 T237 T5 T54 T569 T88	N212 N502 N530	ATP/GTP-binding site motif A (P-loop) A216- S223 Zinc finger C2H2 type domain C238-H258, C266-H286, C294-H314, C322-H342, C350-H370, C378-H398, C406-H426, C434-H454, C462-H482, C490-H510, C518-H538 Zinc finger protein motif: V4-W77 KRAB box domain: V4- W73	g7688669 zinc finger protein ZNF140-like protein [Homo sapiens]	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODROM BLAST_PRODROM BLAST_DOMO
32 1527064	390	S107 S145 S167 S344 S354 S52 T112 T162 T172 T219 T352	N160 N214	Transcription factor domain: V102-E371 Heat shock factor (transcriptional activator) signature: L317-I329	g 532313 NF45 protein Kao, P.N. et al. (1994) J Biol Chem 1994 Aug 12;269:20691- 9	MOTIFS BLAST_GENBANK BLIMPS_PRINTS BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
33 1557491	601	S158 S163 S179 S219 S313 S334 S355 S513 S559 S82 T186 T187 T190 T218 T246 T318 T412 T430 T482 T486 T514 T594 Y75	N2 N104 N484	Zinc finger C2H2 type domain C418-H438, C446-H466, C474-H494, C502-H522, C533-H553	g 220643 zinc finger protein	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS-PRODROM
34 1576862	834	S127 S135 S36 S50 S520 S531 S628 S679 S696 S70 S745 S798 S803 S805 S9 T391 T445 T487 T543 T663 T688 T724 T761 T791		PHD finger: C219-I233 Zinc finger protein motif: C202-R260, L256-H364 Peregrin transcriptional regulator domain: D199-K389, A524-A551	g1510153 similar to human bromodomain protein BR140 Nagase, T. et al. DNA Res 1996 Oct 31;3(5):321-9, 341-54	MOTIFS BLAST_GENBANK BLIMPS_PFAM BLAST_PRODROM BLAST_DOMO
35 1609731	499	S104 S108 S16 S50 S56 S81 T155 T259 T7 Y134	N139	Zinc finger C2H2 type domain: C169-H189, C197-H217, C225-H245, C253-H273, C281-H301, C309-H329, C337-H358, C365-H385, C393-H413, C421-H441, C449-H469, C477-H497 KRAB box domain: Q3- V71	g456269 zinc finger protein 30 Denny, P. and Ashworth, A. (1994) Mamm. Genome 5:643-645	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODROM BLAST_PRODROM BLAST_DOMO
36 1674538	402	S102 S158 S193 S219 S324 S384 T12 T292 T3 T344 T354 Y351	N303 N382	Zinc finger C2H2 type domain: C73-H93, C101- H121, C129-H149, C157- H177, C185-H205, C213- H233, C241-H261, C269- H289 Zinc finger protein domain: E62-H121, Q82-K153, K162-K237, K246-K319	g 55473 zinc finger protein	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLAST_PRODROM BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
37 1675287	579	S134 S22 S270 S347 S57 T176 T222 T293 T526 T535 T537 T82 Y285 Y362		Zinc finger C3HC4 type signature: C400-C408 Zinc finger protein domain: C206-C408	g1136384 C3HC4 containing protein	MOTIFS BLAST_GENBANK BLIMPS_BLOCKS BLAST_PRODOM
38 1693903	426	S12 S231 S290 S328 S360 S381 S63 T114 T318 T408	N246	CCCH-Zinc finger protein motif: C113-H123		MOTIFS BLIMPS-PFAM
39 1702962	266	S78 T127 T163 T171 T196 T261 Y203	N20	Zinc finger C2H2 type domain: F175-H197, H193-C205, E194-H221, C205-H225, H225-H249, P230-S243, F231-H253	g5001720 odd-skipped related 1 protein [Mus musculus] So, P.L. and Danielian, P.S. (1999) Mech. Dev. 84:157-160	MOTIFS BLAST_GENBANK BLAST_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODOM BLAST_DOMO
40 1712916	358	S160 S164 S21 S230 S255 S267 S269 S286 S291 S299 S350 T101 T131 T99 Y97	N228 N238 N249 N284	'Homeobox' domain signature: K74-K129, N95-L106, L106-K129, S110-K129	g 1899230 iroquois- class homeodomain protein IRX-2a	MOTIFS BLAST_GENBANK BLIMPS_BLOCKS BLIMPS_PRINTS BLAST_DOMO
41 1748313	260	S102 S183 S204 S228 S35 S74 T13 T145 T167 T176 T30	N53 N124 N178			MOTIFS
42 1754833	263	S109 S177 S45 S83 S95 T31 T55 T59 T67 T74	N258	Zinc finger C3HC4 type signature: C181-C221, S177-T232	g3790583 RING-H2 finger protein RHC1a	MOTIFS BLAST_GENBANK HMMER_PFAM PROFILESAN
43 1798701	581	S356 S368 S43 S473 S8 T145 T166 T202 T309 T360 T377 T425 T486 T556 T559 T56 T95 Y175	N77 N164 N550		g6688742 putative TH1 protein [Mus musculus]	MOTIFS BLAST_GENBANK
44 1842496	117	S4			g 4336506 transcription elongation factor	MOTIFS BLAST_GENBANK

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
45 1868613	202				g171091 ASF1 [Saccharomyces cerevisiae] DNA repair-associated protein Le, S. et al. (1997) Yeast 13:1029-1042	MOTIFS BLAST_GENBANK BLAST_PRODOM
46 1870609	442	S166 S18 S308 S315 S322 S341 S358 S373 S400 S401 T129 T176 T26 T303 T333 T422	N398	Zinc finger C3HC4 type signature: C140-C177	g5931953 autocrine motility factor receptor [Mus musculus] Shimizu, K. et al. (1999) FEBS Lett. 456:295-300	MOTIFS BLAST_GENBANK BLAST_Pfam
47 1871961	765	S177 S198 S264 S514 S547 S604 S682 T225 T269 T349 T504 T645 T696	N81 N175 N520	Zinc finger C2H2 type domain: C595-H617, C687-H709 GAL 11 transcription factor motif: T347- M627 Coiled coil domain: Q4-Q44, E206-Q428	g6672074 nuclear protein NP94 [Homo sapiens]	MOTIFS BLAST_GENBANK
48 1876258	352	S118 S153 S222 S255 S317 S9 T250 T289 T321		ATP/GTP-binding site motif A (P-loop): A193-T200 Zinc finger C2H2 type domain: C165-H186, C168-S222, C194-H214, C244-H264, C247-Q301, C272-H292, C275-E329, P297-S310, C300-H320, L313-G322, H316-C328, C328-H349, F323-K352	g 4165083 growth factor independence-1B (transcription factor expressed in t- lymphocytes) B. Rodel et al. Genomics 1998 Dec 15;54(3):580-2	MOTIFS BLAST_GENBANK HMMER_Pfam BLIMPS_BLOCKS BLIMPS_PRODOM BLAST_PRODOM BLAST_DOMO

Table 2 (cont.)

Polyptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
49 1929822	1102	S1001 S1008 S1051 S1067 S11 S346 S365 S425 S740 S805 S82 S874 S891 S921 S934 S953 S955 S970 S982 T142 T171 T18 T443 T488 T51 T52 T520 T661 T782 T995 Y764 Y818	N50 N132 N315 N398 N439 N486 N674 N857 N887 N951 N1030 N1049 N1066 N1079	Homeobox domain: L771- R813 Zinc finger C2H2 type domain: C514-H536 Glutaredoxin active site: C514-V524	g4406073 activity- dependent neuroprotective protein (contains a glutaredoxin active site) Bassan, M. J Neurochem 1999 Mar;72(3):1283-93	MOTIFS BLAST_GENBANK BLIMPS_BLOCKS
50 1970095	121	T25 S32 T39 T63 S72 S91	N26		g5713279 Yippee protein [Drosophila melanogaster]	MOTIFS BLAST_GENBANK
51 1975473	233	T34 S8 S25 S65 T174 S199	N26	Signal peptide: M1- A62 Myc-type 'helix-loop- helix' dimerization domain signature: L7- T63, V11-P122, R31- Q85, E39-H54, S65-Q85 FOS-type leucine zipper: L84-L105	g4704419 WS basic-helix-loop- helix leucine zipper protein [Homo sapiens] Meng, X. et al. (1998) Human Genetics 103:590-599	MOTIFS BLAST_GENBANK HMMER_Pfam BLIMPS_BLOCKS BLAST_DOMO
52 1976527	147	T63 S71 T114 S122	N28 N65	Signal peptide: M1- A52 NFYB transcription factor subunit: R4-K100, P5-R94, K20- M76 CCAAT-binding transcription factor motif: A56-R93, E6- D111	g9623363 DNA polymerase epsilon p17 subunit [Homo sapiens] Li, Y. et al. (2000) J. Biol. Chem. 275:23247-23252	MOTIFS BLAST_GENBANK PROFILES SCAN BLIMPS_BLOCKS BLIMPS_PRINTS BLAST_PRODOME BLAST_DOMO
53 2108023	96	T32 T7 S13 T50 T56 S73	N36		g9294739 bithoraxoid-like protein [Homo sapiens]	MOTIFS BLAST_GENBANK

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
54 2135746	259	S56 S120 S166 S181 S233 S23 S29 S89 T208		Signal peptide: M1-G20		MOTIFS SPSCAN
55 2154810	474	S88 S156 S50 S56 T80 T84 T124 S140 S145 Y94	N38 N97	Zinc finger C2H2 type domain: C172-H192, C200-H220, C228-H248, C256-H276, C284-H304, C312-H332, C340-H360, C368-H388, C396-H416 Zinc finger protein motif: F8-G46 KRAB box domain: S5- Y75	g456269 zinc finger protein 30	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODOR BLAST_PRODOR BLAST_DOMO
56 2228991	231	T167 S213 T99 S186 T223 S10 S35 S67 T99	N97	Signal peptide: M1-I29 Prenyl group binding site (CAAX box) T228-D231 Zinc finger domain: C166-H176		MOTIFS SPSCAN BLIMPS_PFAM
57 2241206	456	S37 S404 S406 T183 T205 T212 T264 T295 T300 T352 T50 T72	N430	RNA-binding RGG-box domain I392-G452	g 1177636 transcriptional activator SPO8	MOTIFS BLAST_GENBANK BLAST_DOMO
58 2259590	159	S87 T96 S11 S24 S25 T118 T146		Zinc finger protein motif: F88-G126 KRAB box domain: V86- C156	g506502 NK10 Zinc finger repressor protein [Mus musculus] 2.9e-15 47&ID aa 75- 159 Lange, R. et al. DNA Cell Biol 1995 Nov;14(11):971-81	MOTIFS BLAST_GENBANK BLIMPS_PRODOR BLAST_PRODOR BLAST_DOMO
59 2307537	260	T66 S124 S182 S197 T7 S56 S77	N36 N195		g4325209 endocrine regulator	MOTIFS BLAST_GENBANK

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
60	2440675 352	S118 S153 S222 S255 S317 S9 T250 T289 T321		A193 ATP/GTP-binding site motif A (P-loop) A193-T201 zinc finger C2H2 type domain C165-H186 C194-H215, C244-H265, C272-H293, C300-H321, C328-H349	g 4165083 growth factor independence-1B zinc finger protein Rodel, B. et al. Genomics 1998 Dec 15;54(3):580-2	MOTIFS BLAST_GENBANK BLIMPS_PRINTS BLIMPS_PRODUM BLAST_DOMO
61	2463542 467	S126 S132 S200 S214 S220 S249 S393 S404 S419 S42 S430 S435 S449 S77 T105 T14 T253 T397 T454 T81 Y313	N114 N335 N354	Zinc finger C2H2 type domain: C6-H28		MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS
62	2486031 550	S115 S272 S317 S429 S441 S444 S62 S81 T302 T360 T364	N238 N249	Homeobox domain: L70- I112	g 1504088 DNA-binding protein	MOTIFS BLAST_GENBANK BLIMPS_BLOCKS
63	2493052 450	S272 S293 S368 S41 S411 S413 T108 T232 T238 T374 T409 T418 T433 T50 Y262 Y396 Y99	N122 N167 N185 N403	Signal peptide: M1-S32 Cytochrome c family heme-binding site: C359-V364 Zinc finger C2H2 type domain: C226-H248, C357-H381	g9230649 zinc finger protein 277 [Homo sapiens] Liang, H. et al. (2000) Genomics 66:226-228	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS
64	2512074 378	S132 S3 T9 T18 S77 S328 T182 S197 T279 S365	N120 N150 N180 N255 N310	Zinc finger C2H2 type domain: C161-H181, C189-H209, C217-H237, C245-H265, C273-H293, C301-H321, C329-H349, C357-H377 Zinc finger protein domain: F10-G48 KRAB box domain: Q5- P79	g 881564 ZNF157	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
65 2646274	233	S14 T34 T127	N53 N67	Protein I transcription initiation factor F84- Y230	g10046714 transcription initiation factor IA protein [Homo sapiens]	MOTIFS BLAST_GENBANK BLAST_PRODOM
66 2672566	102	T66	N11 T99		g 322032 polyhomeotic Z protein Hemenway, C.S. et al. (1998) Oncogene 16:2541-2547 Haluska, P. et al. (1999) Nucleic Acids Res. 27:2538-2544	MOTIFS
67 2689674	287	T25 T232 S32 S122		Eukaryotic putative RNA-binding region RNP-1 signature: K137- D146, L98-F116 RNA recognition motif: L98-L170, L5-K77	g 1899188 DNA binding protein ACBF AC-rich binding factor	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLAST_PRODOM BLAST_DOMO
68 2703282	208	S11 S23 S117 Y124			g5712754 sex comb on midleg- like-1 protein [Homo sapiens] van de Vosse, E. et al. (1998) Genomics 49:96-102	MOTIFS BLAST_GENBANK
69 2738293	177	S71 T43 S5 T115			g11907923 enhancer of polycomb [Homo sapiens] Shimono, Y. et al. (2000) J. Biol. Chem. 275:39411-39419	MOTIFS BLAST_GENBANK

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
70 2772776	179	T173 S29 S39 T63 T106		Zinc finger protein motif: P104-A166	g6942207 PPARG gamma cofactor 2 [Mus musculus] Castillo, G.C. et al. (1999) EMBO J. 18:3676-3687	MOTIFS BLAST_GENBANK BLAST_PRODUM BLAST_DOMO
71 2774476	212	S132 S159 S196 S20 S201 S31 S45 T136 T205 T68		RBP-J Kappa Recombination signal motif: P39-D206	g 2052119 transcription factor RBP-L	MOTIFS BLAST_GENBANK BLAST_PRODUM
72 2804624	256	S103 S202 S238 S244 S33 S7 S85 S89 T112 T212 T245 T99	N6 N101 N132	MAF-1 nuclear matrix protein motif: G82- T210	g3786409 contains similarity to Saccharomyces cerevisiae MAF-1 protein	MOTIFS BLAST_GENBANK BLAST_PRODUM
73 2848225	475	S179 S180 S239 S24 S295 S378 S434 T14 T142 T164 T282 T332 T36 Y136 Y268	N12 N93	Zinc finger C2H2 type domain: F6-R44, C171- Q191, C199-H219, C227- H247, C255-H275, C283- H303, C311-H331, C339- H358, C366-H386, C394- H415, C422-H442, C450- H470 Zinc finger 136: W37- Q145 Zinc finger 137: S259- R335 KRAB box: M1-D76	g 930123 zinc finger protein	MOTIFS BLAST_GENBANK HMMER_PFBM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM BLAST_PRODUM BLAST_DOMO
74 2882241	206	S164 S166 S57 S161 Y29		Helix-loop-helix DNA- binding domain: G58- E110, H27-D165 Myc-type helix-loop- helix motif: E66-K81, C90-E110	g 1184157 Max- interacting transcriptional repressor	MOTIFS BLAST_GENBANK BLAST_PFBM BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
75 2939011	596	S152 S203 S212 S244 S272 S477 S481 S516 S536 T121 T164 T200 T204 T229 T339 T361 T363 T396 T537 T543	N84 N510		g 5081374 glucocorticoid modulatory element binding protein-1	MOTIFS BLAST_GENBANK
76 2947188	644	S116 S207 S22 S403 S488 S85 T110 T487 T52 T612	N66 N190 N265 N376	ATP/GTP-binding site motif A (P-loop): G142-S149 Zinc finger C2H2 type domain: C199-H219, C227-H247, C255-H275, C283-H303, C311-H331, C339-H359, C367-H387, C395-H415, C423-H443, C451-H471, C479-H499, C507-H527, C535-H555, C563-H583, C591-H611, C619-H639	g5441615 zinc finger protein	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM BLAST_PRODUM
77 3094001	194	T59 T110 S27 S32 S183 Y65	N17	SSU72 start-site selection protein: M1- F194	g4156162 similar to yeast SSU72	MOTIFS BLAST_GENBANK BLAST_PRODUM
78 3110061	536	S21 S134 T157 S214 T76 S83 S252 S404 S462	N132 N380 N389 N445	Zinc finger C2H2 type domain: C202-H222, C230-H250, C258-H277, C286-H306, C314-H334, C342-H362, C370-H390, C398-H418, C426-H446, C454-H474, C482-H502 Transcription factor GATA zinc finger signature: T223-S240 Zinc finger signature: F13-G51, H330-C342	g1017722 repressor transcriptional factor	MOTIFS BLAST_GENBANK HMMER_PFAM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM BLAST_PRODUM BLAST_DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
79 3146614	412	S184 T158 T247 S402		Signal peptide: M1-R29 transcription regulation protein domain: F3-L220 Leucine zipper motif: L80-L101	g2370560 putative translational repressor	MOTIFS BLAST_GENBANK SPSCAN BLAST_PRODUM
80 3295381	482	S161 S216 S318 S352 S385 S408 S456 S72 S99 T177 T18 T84 T88 T9 T94		Zinc finger C2H2 type domain: C178-H198, C206-H226, C234-H254, C262-H282, C290-H310, C346-H366, C374-H394, C402-H422 Zinc finger signature: F10-G48 KRAB box: V8-G69	g6118383 zinc finger protein ZNF223 [Homo sapiens]	MOTIFS BLAST_GENBANK BLAST_PFBM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM BLAST_PRODUM BLAST_DOMO
81 3364774	554	S134 S183 S269 S292 S307 S458 S514 S62 S94 T125 T16 T325 T402 T497	N467	ATP/GTP-binding site motif A (P-loop): A505-S512 Zinc finger C2H2 type domain: C310-H330, C338-H358, C366-H386, C394-H414, C422-H442, C450-H470, C478-H498, C506-H526 KRAB box: V124-S183 Zinc finger signature: F126-P164	g 3818515 zinc finger protein ZNF210	MOTIFS BLAST_GENBANK BLAST_PFBM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRODUM BLAST_PRODUM BLAST_DOMO
82 3397777	488	S171 S235 S244 S271 S346 S356 S417 S42 T153 T178 T185	N448	Zinc finger C3HC4 type signature: C30-I40, C15-C59, V9- S64 Interleukin 2 transcription down- regulatory domain: T130-W333 RFP Transforming protein: H67-G347	g11022688 interferon-responsive finger protein 1 middle form [Homo sapiens] Orimo, A. et al. (2000) Genomics 69:143-149	MOTIFS BLAST_GENBANK HMMER_PFBM BLIMPS_BLOCKS PROFILESSCAN BLIMPS_PFBM BLAST_PRODUM BLAST_DOMO

Table 2 (cont.)

Polyptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
83 3403046	127	T57 S31 S52		Signal peptide: M1-P19 bZIP transcription factors basic domain signature: R40-K55, E33-E97 FOS transforming protein: Q28-K44, N45- D61, L63-L84 DNA-binding transcription factor: A17-L104 Leucine zipper motifs: L63-L84, L70-L91	g 1890635 Jun dimerization protein 1 JDP-1	MOTIFS BLAST_GENBANK HMMER-PFAM BLIMPS_BLOCKS BLAST_PRODUM BLAST_DOMO
84 3538506	532	S143 S170 S185 S191 S282 S283 S327 S340 S457 S49 S497 S72 S99 T147 T156 T223 T30 T331 T449 T501 T71 T86	N280	Signal peptide: M1- A51 C2H2 Zn finger domain: C3-H23, C109-H129, C293-H313, C463-H483, C3-H19	g4056411 Human homolog of Mus musculus wizS protein	MOTIFS BLAST_GENBANK SPSCAN HMMER-PFAM BLIMPS-BLOCKS MOTIFS
85 3575519	353	S110 S194 S210 S240 S256 S266 S285 T189 T198 T278 T326 T60 T77		C3HC4 Zn finger domain: C23-C78, C39- A48, K19-G88 RFP (Zn finger oncogenic protein): K106-K291	g9945010 RING-finger protein MURF [Mus musculus] Spencer, J.A. et al. (2000) J. Cell Biol. 150:771-784	MOTIFS BLAST_GENBANK HMMER-PFAM PROFILESSCAN BLAST-DOMO MOTIFS
86 3598694	407	S16 S76 S151 S315 T390			g 5668703 XDRP1	MOTIFS BLAST_GENBANK BLIMPS-BLOCKS
87 3638819	350	S199 S212 S236 Y156 Y184	N12 N210	Transmembrane domain: L310-F330 C2H2 Zn finger domain: G82-A264, Y114-H136, C88-H108, Y142-H164, F170-H192, Y198-H220, F226-H248, P113-S126, L129-G138	g1020145 DNA binding protein	MOTIFS BLAST_GENBANK HMMER BLIMPS-PRINTS BLAST-PRODUM BLAST-DOMO MOTIFS

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
88 3717139	215	S108 S198 S70 T193	N42 N196	Homeobox domain: K33- N96, Q36-E95, E50- A112, R79-N96, T58- L69, L73-R92	g 2632119 Splice variant of homeobox gene Prx3A alternative N-terminal region	MOTIFS BLAST_GENBANK HMMER-PFAM PROFILES-SCAN BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO
89 3892962	489	S227 S43 S113 T230 T97 S196 T392	N110 N200 N308 N319 N366 N450 N480	C2H2 Zn finger domain: C132-H152, L145-G154, C160-H180, C188-H208, C216-H236, C244-H264, C272-H292, C300-H320, P325-S338, C328-H348, C356-H376, C384-H404, C412-H432, C440-H460, C468-H488, G108-H488 Zn finger protein domain: K127-H488	g 488555 zinc finger protein ZNF135	MOTIFS BLAST_GENBANK HMMER-PFAM BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO
90 4153521	399	S112 S14 S146 S157 S164 S176 S364 S70 S75 S83 T119 T123 T133 T202 T5 T84	N139 N155 N177 N184	C2H2 Zn finger domain: C315-H335, C231-H251, C343-H363, C287-H307, C203-H223, C259-H279, P340-S353, L216-G225, C371-H391 Zn finger protein domain: V4-W77, F6- G44 KRAB box domain: S2- W73, V4-D72	g7688669 zinc finger protein ZNF140-like protein [Homo sapiens]	MOTIFS BLAST_GENBANK HMMER-PFAM BLIMPS-BLOCKS BLIMPS-PRINTS BLIMPS-PRODOM BLAST-DOMO
91 4585038	309	S106 S270 S293 S51 S52 S75 S94 T132 T172 T198 T205 T237 T301 T31 T40 T57		transcriptional repressor DNA binding signature: D45-K275	g 4960159 GC-rich sequence DNA-binding factor candidate	MOTIFS BLAST_GENBANK BLAST-PRODOM
92 4674640	361	S28 S30 S352 S56 T170 T176 T206 T77 Y233 Y68	N288	Type I antifreeze protein signature: Q253-F270	g 3779240 zinc finger protein	MOTIFS BLAST_GENBANK BLIMPS-PRINTS

Table 2 (cont.)

Polyptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
93 4676066	540	S115 S135 S151 S202 S301 S34 S39 S405 S490 S497 T368 T508	N222	Signal peptide: M1- S29 RFP (Zn finger oncogenic protein): R381-I526 Adrenomedullin signature: R111-A128	g 3916727 estrogen- responsive B box protein	MOTIFS BLAST_GENBANK SPSCAN BLIMPS_PRINTS BLAST-DOMO
94 4830687	84			Signal peptide: M1- A66 C3HC4 Zn finger domain: C33-E79, C51- C76, N19-K81 Glycoprotein hormone signature: M1-H58	g7649253 hepatocellular carcinoma associated ring finger protein [Homo sapiens]	MOTIFS BLAST_GENBANK HMMER_PFBM SPSCAN PROFILES SCAN BLAST-DOMO
95 4880891	1312	S105 S1060 S1063 S1067 S1128 S1129 S1135 S1153 S1159 S1181 S1208 S1222 S1249 S157 S158 S159 S17 S216 S274 S276 S295 S296 S47 S471 S483 S527 S591 S595 S656 S666 S680 S712 S713 S717 S736 S750 S758 S815 S860 S861 S862 S888 S945 S947 T100 T1025 T1034 T1046 T1228 T126 T1293 T140 T31 T41 T481 T507 T508 T531 T793 T801 T811 T812 T876 T939 T971 Y655 Y75 Y89 Y9	N294 N432 N755 N856 N859 N910 N1151 N1226	ARID (AT-Rich Interaction Domain) DNA binding domain: E303-V413 Retinoblastoma binding protein: T742-R1312	g 5257005 Rb binding protein homolog	MOTIFS BLAST_GENBANK HMMER-PFBM BLAST-PRODOM BLAST-DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
96 4909754	504	S109 S181 S304 S357 S36 S384 S389 S417 T194 T212 T246 T255 T323 T333 T365 T490 Y221 Y262 Y85	N309 N355 N421	Transcription factor- like domain: T20-L120 Lymphoid transcription factor ENL: P10-N209 P245 purinoceptor signature: F121-K131	g476099 transcription factor LSF	MOTIFS BLAST_GENBANK BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO
97 4911931	227	T190 S191 T157 Y62		Transcription factor- like domain: T20-L120 Lymphoid transcription factor ENL: P10-N209 P245 purinoceptor signature: F121-K131	g3878581 Similar to Human AF-9 leukemia protein	MOTIFS BLAST_GENBANK BLAST-PRODOM BLAST-DOMO
98 4920433	233	S43 S50 T62 S77 S110 S131 T165 S17 T69 S194 Y191	N122 N192	Signal peptide: M1- A33 LysR helix-turn helix domain: T97-N122		SPSCAN MOTIFS
99 5042113	511	S176 S203 S276 S278 S430 S436 S455 S56 S99 T12 T173 T239 T247 T274 T372 T449 T504 T509 Y79		Signal peptide: M1- A34 Brain natriuretic peptide: A481-Q499		MOTIFS SPSCAN BLIMPS-PRINTS
100 5083853	247	S102 S110 S123 S19 S190 S58 S84 T150 T163 T212		C-type natriuretic peptide: S44-D54	g 4519621 OASIS (transcription factor) protein	MOTIFS BLAST_GENBANK
101 5283981	276	S160 T68 T126 T168 T193	N20	C2H2 Zn finger domain: K170-H190, F172-H194, C174-H194, L187-D196, E191-H246, Y200-H222, F228-H250, C202-H218, S223-Q252, P227-S240. C230-H250	g 5001720 odd-skipped related 1 protein	MOTIFS BLAST_GENBANK HMMER-PFAM BLIMPS-BLOCKS BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO

Table 2 (cont.)

Polypeptide SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Motifs and Domains	Homologous Sequences	Analytical Methods and Databases
102 5510549	220	S66 T144 S173 T67 S153	N202	C3HC4 Zn finger domain: C168-C208, E164-A219, C168-D211	g9759106 contains similarity to C3HC4-type RING zinc finger protein Sato, S. et al. (1997) DNA Res. 4:215-230	MOTIFS BLAST_GENBANK HMMER-PFAM PROFILES-SCAN BLAST-DOMO
103 5544862	608	S16 S25 S326 S401 S416 S423 S424 S44 S481 S51 S517 S518 S530 S543 S553 S566 S574 S597 T118 T182 T256 T402 T437 T494 Y552 Y579	N29 N251 N538	Small proline rich protein DNA binding signature: E48-P57, P230-P238 Leucine zipper: L63- L84		MOTIFS BLIMPS-PRINTS
104 5573394	653	G650 S299 S371 S499 S552 S593 S599 S78 T240 T262 T270 T300 T381 T432 T525 T53 T57 T9	N115 N220 N293 N597	Nonstructural polyprotein domain: L118-K284		MOTIFS BLAST_DOMO
105 5850840	154	T9 S19 S25 T30 T63 S138 S149 S21 S92		C3HC4 Zn finger domain: C99-C139, K95- S150	g 3873857 similar to C3HC4 type zinc finger	MOTIFS BLAST_GENBANK HMMER-PFAM PROFILES-SCAN
106 5942936	337	T8 S10 S12 S67 T77 S138 T214 S84 T162	N25 N65	Helix-loop-helix DNA binding domain: R49- E132, K51-Q104, E57- R72, S84-Q104, E88- L103	g 5059323 hairy and enhancer of split related-1	MOTIFS BLAST_GENBANK HMMER-PFAM BLIMPS-BLOCKS BLAST-DOMO
107 5951431	535	S152 S201 S212 S254 S256 S287 S348 S351 S354 S378 S385 S409 S414 S428 S475 S527 T22 T418 T66 T98 Y210 Y459	N6 N87 N137	Signal peptide: M1- R54 GATA-type Zn finger domain: A19-W74, M1- H95	g9651765 zinc finger protein 289 [Mus musculus]	MOTIFS BLAST_GENBANK HMMER-PFAM SPSCAN BLAST-PRODOM BLAST-DOMO

Table 3

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
108	095210 Reproductive (0.257) Hematopoietic/Immune (0.200) Nervous (0.171)	Cancer (0.429) Inflammation (0.257) Cell Proliferation (0.143)	PBLUESCRIPT
109	157953 Reproductive (0.293) Hematopoietic/Immune (0.207) Gastrointestinal (0.172)	Cancer (0.483) Cell Proliferation (0.310) Inflammation (0.224)	PBLUESCRIPT
110	159196 Reproductive (0.296) Cardiovascular (0.222) Hematopoietic/Immune (0.111) Gastrointestinal (0.111) Urologic (0.111)	Cancer (0.444) Inflammation (0.370) Cell Proliferation (0.222)	PBLUESCRIPT
111	343338 Hematopoietic/Immune (0.300) Nervous (0.260) Reproductive (0.140)	Cancer (0.380) Inflammation (0.320) Cell Proliferation (0.220)	PBLUESCRIPT
112	402386 Hematopoietic/Immune (0.381) Reproductive (0.190) Gastrointestinal (0.143) Nervous (0.143)	Inflammation (0.476) Cancer (0.333)	PBLUESCRIPT
113	456487 Reproductive (0.248) Nervous (0.198) Gastrointestinal (0.132)	Cancer (0.488) Inflammation (0.207) Cell Proliferation (0.165)	PBLUESCRIPT
114	490256 Developmental (0.231) Reproductive (0.231) Endocrine (0.154) Hematopoietic/Immune (0.154) Gastrointestinal (0.154)	Cancer (0.231) Cell Proliferation (0.231) Inflammation (0.231)	PBLUESCRIPT
115	494740 Gastrointestinal (0.209) Nervous (0.209) Hematopoietic/Immune (0.186)	Inflammation (0.395) Cancer (0.302) Cell Proliferation (0.209)	PBLUESCRIPT
116	507475 Reproductive (0.246) Hematopoietic/Immune (0.180) Gastrointestinal (0.148)	Cancer (0.426) Cell Proliferation (0.230) Inflammation (0.230)	PBLUESCRIPT
117	531581 Hematopoietic/Immune (0.231) Reproductive (0.231) Nervous (0.154)	Cancer (0.385) Cell Proliferation (0.231) Inflammation (0.205)	PSPORT1

Table 3 (cont.)

Nucleotide ID No.	SEQ ID No.	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
118	675190	Reproductive (0.389) Nervous (0.278) Cardiovascular (0.111) Urologic (0.111)	Cancer (0.722) Inflammation (0.111) Trauma (0.111)	PSPORT1
119	685434	Reproductive (0.333) Nervous (0.194) Cardiovascular (0.111) Hematopoietic/Immune (0.111)	Cancer (0.556) Inflammation (0.278) Cell Proliferation (0.111)	PSPORT1
120	788663	Reproductive (0.303) Cardiovascular (0.182) Hematopoietic/Immune (0.152)	Cancer (0.455) Inflammation (0.303) Cell Proliferation (0.212)	PSPORT1
121	870100	Reproductive (0.298) Nervous (0.170) Cardiovascular (0.128)	Cancer (0.660) Inflammation (0.170) Cell Proliferation (0.149)	PSPORT1
122	879500	Reproductive (0.203) Gastrointestinal (0.153) Hematopoietic/Immune (0.136)	Cancer (0.373) Inflammation (0.322) Cell Proliferation (0.203)	PSPORT1
123	975377	Reproductive (0.215) Nervous (0.177) Hematopoietic/Immune (0.152)	Cancer (0.418) Inflammation (0.291) Cell Proliferation (0.127)	PSPORT1
124	1208721	Reproductive (0.282) Nervous (0.200) Hematopoietic/Immune (0.141)	Cancer (0.471) Inflammation (0.282) Cell Proliferation (0.141)	PSPORT1
125	1234329	Reproductive (0.277) Nervous (0.191) Cardiovascular (0.128) Hematopoietic/Immune (0.128)	Cancer (0.553) Cell Proliferation (0.234) Inflammation (0.213)	pINCY
126	1238747	Hematopoietic/Immune (0.283) Gastrointestinal (0.167) Reproductive (0.150)	Cancer (0.400) Inflammation (0.300) Trauma (0.117) Cell Proliferation (0.117)	PSPORT1
127	1265980	Nervous (0.900) Developmental (0.100)	Cell Proliferation (0.400) Inflammation (0.200) Neurological (0.200)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
128	1297333 Developmental (0.273) Reproductive (0.273) Hematopoietic/Immune (0.273)	Cell Proliferation (0.273) Inflammation (0.273) Cancer (0.182)	pINCY
129	1312824 Reproductive (0.238) Hematopoietic/Immune (0.222) Gastrointestinal (0.159)	Cancer (0.429) Inflammation (0.238) Cell Proliferation (0.175)	pINCY
130	1359294 Reproductive (0.219) Nervous (0.157) Gastrointestinal (0.145)	Cancer (0.438) Inflammation (0.247) Cell Proliferation (0.188)	pINCY
131	1377380 Reproductive (0.385) Developmental (0.231) Hematopoietic/Immune (0.231)	Cancer (0.538) Cell Proliferation (0.385) Inflammation (0.154)	pINCY
132	1383473 Reproductive (0.318) Nervous (0.182) Hematopoietic/Immune (0.121)	Cancer (0.515) Inflammation (0.288) Cell Proliferation (0.197)	pINCY
133	1388860 Cardiovascular (0.167) Nervous (0.167) Reproductive (0.167)	Cancer (0.444) Inflammation (0.222) Cell Proliferation (0.167) Trauma (0.167)	pINCY
134	1395322 Nervous (0.261) Reproductive (0.261)	Cancer (0.478) Inflammation (0.304) Cell Proliferation (0.130) Trauma (0.130)	pINCY
135	1419370 Reproductive (0.290) Nervous (0.246) Gastrointestinal (0.116)	Cancer (0.522) Cell Proliferation (0.188) Inflammation (0.130)	pINCY
136	1429773 Reproductive (0.255) Gastrointestinal (0.160) Cardiovascular (0.128)	Cancer (0.521) Inflammation (0.191) Cell Proliferation (0.170)	pINCY
137	1470820 Reproductive (0.231) Developmental (0.154) Gastrointestinal (0.154) Hematopoietic/Immune (0.154) Nervous (0.154) Gastrointestinal (0.154)	Cancer (0.385) Cell Proliferation (0.231) Inflammation (0.231)	pINCY

Table 3 (cont.)

Nucleotide ID	SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
138	1483455	Nervous (0.222) Urologic (0.156) Cardiovascular (0.111) Developmental (0.111) Reproductive (0.111)	Cancer (0.422) Cell Proliferation (0.244) Inflammation (0.244)	pINCY
139	1527064	Reproductive (0.262) Nervous (0.169) Cardiovascular (0.131)	Cancer (0.481) Cell Proliferation (0.257) Inflammation (0.224)	PBLUESCRIPT
140	1557491	Nervous (0.222) Reproductive (0.222) Cardiovascular (0.167)	Cancer (0.444) Neurological (0.167) Cell Proliferation (0.111) Inflammation (0.111)	pINCY
141	1576862	Gastrointestinal (0.280) Hematopoietic/Immune (0.240) Nervous (0.160)	Cancer (0.480) Inflammation (0.320) Cell Proliferation (0.120)	pINCY
142	1609731	Gastrointestinal (0.286) Nervous (0.286) Cardiovascular (0.143) Developmental (0.143) Urologic (0.143)	Cancer (0.429) Cell Proliferation (0.286) Neurological (0.143) Trauma (0.143)	pINCY
143	1674538	Nervous (0.364) Cardiovascular (0.364) Gastrointestinal (0.182)	Cancer (0.364) Cell Proliferation (0.182)	pINCY
144	1675287	Reproductive (0.373) Hematopoietic/Immune (0.169) Urologic (0.119)	Cancer (0.492) Inflammation (0.305) Cell Proliferation (0.153)	pINCY
145	1693903	Reproductive (0.212) Hematopoietic/Immune (0.186) Nervous (0.177)	Cancer (0.434) Inflammation (0.327) Cell Proliferation (0.257)	pINCY
146	1702962	Reproductive (0.389) Cardiovascular (0.167) Gastrointestinal (0.167)	Cancer (0.556) Trauma (0.222)	pINCY
147	1712916	Reproductive (1.000)	Cancer (1.000)	pINCY
148	1748313	Nervous (0.265) Reproductive (0.162) Hematopoietic/Immune (0.147)	Cancer (0.456) Inflammation (0.279) Cell Proliferation (0.176)	pINCY

Table 3 (cont.)

Nucleotide ID NO:	SEQ	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
149	1754833	Hematopoietic/Immune (0.208) Gastrointestinal (0.189) Nervous (0.151)	Inflammation (0.377) Cancer (0.358) Cell Proliferation (0.170)	pINCY
150	1798701	Nervous (0.237) Reproductive (0.212) Gastrointestinal (0.119)	Cancer (0.449) Inflammation (0.237) Cell Proliferation (0.178)	pINCY
151	1842496	Reproductive (0.254) Nervous (0.187) Gastrointestinal (0.119)	Cancer (0.500) Cell Proliferation (0.224) Inflammation (0.149)	PSORT1
152	1868613	Hematopoietic/Immune (0.286) Reproductive (0.257) Cardiovascular (0.114) Gastrointestinal (0.114)	Cell Proliferation (0.486) Cancer (0.400) Inflammation (0.286)	pINCY
153	1870609	Nervous (0.207) Reproductive (0.195) Gastrointestinal (0.159)	Cancer (0.439) Inflammation (0.244) Cell Proliferation (0.171)	pINCY
154	1871961	Reproductive (0.268) Nervous (0.196) Hematopoietic/Immune (0.113)	Cancer (0.474) Cell Proliferation (0.247) Inflammation (0.165)	pINCY
155	1876258	Hematopoietic/Immune (0.600) Cardiovascular (0.200) Reproductive (0.100) Gastrointestinal (0.100)	Inflammation (0.400) Trauma (0.200) Cancer (0.100)	pINCY
156	1929822	Reproductive (0.255) Nervous (0.160) Hematopoietic/Immune (0.128) Gastrointestinal (0.128)	Cancer (0.479) Inflammation (0.223) Cell Proliferation (0.213)	pINCY
157	1970095	Nervous (0.205) Reproductive (0.205) Cardiovascular (0.133)	Cancer (0.385) Inflammation (0.256) Cell Proliferation (0.159)	PBLUESCRIPT
158	1975473	Gastrointestinal (0.464) Reproductive (0.250)	Cancer (0.536) Inflammation (0.214) Cell Proliferation (0.179)	pINCY
159	1976527	Reproductive (0.247) Gastrointestinal (0.192) Nervous (0.178)	Cancer (0.466) Inflammation (0.247) Cell Proliferation (0.233)	pINCY

Table 3 (cont.)

Nucleotide ID	SEQ ID NO.	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
160	2108023	Reproductive (0.750) Nervous (0.250)	Cancer (0.500) Inflammation (0.250) Trauma (0.250)	PSPORT1
161	2135746	Nervous (0.321) Cardiovascular (0.214) Reproductive (0.143)	Cancer (0.500) Inflammation (0.214) Trauma (0.179)	pINCY
162	2154810	Cardiovascular (0.222) Developmental (0.222) Hematopoietic/Immune (0.222)	Cancer (0.333) Cell Proliferation (0.333) Inflammation (0.222)	pINCY
163	2228991	Hematopoietic/Immune (0.500) Gastrointestinal (0.167) Reproductive (0.167)	Inflammation (0.333) Cancer (0.250) Cell Proliferation (0.167)	pINCY
164	2241206	Cardiovascular (0.269) Gastrointestinal (0.154) Nervous (0.154)	Cancer (0.346) Cell Proliferation (0.346) Inflammation (0.308)	pINCY
165	2259590	Reproductive (0.375) Urologic (0.250) Hematopoietic/Immune (0.125) Developmental (0.125) Endocrine (0.125)	Cancer (0.500) Cell Proliferation (0.250) Inflammation (0.250)	PSPORT1
166	2307537	Reproductive (0.241) Gastrointestinal (0.138) Nervous (0.138)	Cancer (0.414) Cell Proliferation (0.241) Inflammation (0.241)	PSPORT1
167	2440675	Hematopoietic/Immune (0.600) Cardiovascular (0.200) Reproductive (0.100) Gastrointestinal (0.100)	Inflammation (0.400) Trauma (0.200) Cell Proliferation (0.100) Cancer (0.100)	pINCY
168	2463542	Reproductive (0.333) Nervous (0.250) Hematopoietic/Immune (0.125)	Cancer (0.542) Inflammation (0.292) Trauma (0.125)	pINCY
169	2486031	Reproductive (0.333) Cardiovascular (0.167) Gastrointestinal (0.167) Nervous (0.167)	Cancer (0.333) Cell Proliferation (0.250)	pINCY

Table 3 (cont.)

Nucleotide ID	SEQ ID NO.	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
170	2493052	Nervous (0.200) Gastrointestinal (0.171) Reproductive (0.171)	Cancer (0.429) Cell Proliferation (0.343) Inflammation (0.229)	pINCY
171	2512074	Hematopoietic/Immune (0.333) Reproductive (0.333) Nervous (0.250)	Inflammation (0.500) Cancer (0.417) Cell Proliferation (0.333)	pINCY
172	2646274	Gastrointestinal (0.207) Reproductive (0.207) Developmental (0.138)	Cancer (0.379) Inflammation (0.310) Cell Proliferation (0.207)	pINCY
173	2672566	Nervous (0.400) Gastrointestinal (0.200) Cardiovascular (0.100) Hematopoietic/Immune (0.100) Reproductive (0.100)	Cancer (0.600) Cell Proliferation (0.100) Inflammation (0.100) Neurological (0.100)	pINCY
174	2689674	Gastrointestinal (0.191) Reproductive (0.191) Hematopoietic/Immune (0.170)	Cancer (0.489) Inflammation (0.191) Cell Proliferation (0.149)	pINCY
175	2703282	Reproductive (0.409) Nervous (0.136) Gastrointestinal (0.114) Hematopoietic/Immune (0.114)	Cancer (0.409) Inflammation (0.386) Cell Proliferation (0.205)	pINCY
176	2738293	Reproductive (0.333) Cardiovascular (0.167) Gastrointestinal (0.167)	Cancer (0.416) Cell Proliferation (0.167) Inflammation (0.167) Trauma (0.167)	pINCY
177	2772776	Reproductive (0.232) Gastrointestinal (0.152) Nervous (0.134)	Cancer (0.500) Inflammation (0.205) Cell Proliferation (0.152)	pINCY
178	2774476	Gastrointestinal (0.712) Developmental (0.143) Nervous (0.143)	Trauma (0.429) Cancer (0.286) Cell Proliferation (0.286)	pINCY
179	2804624	Reproductive (0.252) Gastrointestinal (0.173) Cardiovascular (0.150)	Cancer (0.480) Inflammation (0.236) Trauma (0.134)	pINCY

Table 3 (cont.)

Nucleotide ID NO:	SEQ	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
180	2848225	Reproductive (0.385) Hematopoietic/Immune (0.231) Gastrointestinal (0.154)	Cancer (0.385) Trauma (0.308) Cell Proliferation (0.154) Inflammation (0.154)	pINCY
181	2882241	Hematopoietic/Immune (0.259) Gastrointestinal (0.185) Reproductive (0.185)	Cancer (0.519) Inflammation (0.333) Cell Proliferation (0.148)	pINCY
182	2939011	Hematopoietic/Immune (0.263) Cardiovascular (0.158) Gastrointestinal (0.158) Urologic (0.158) Nervous (0.158)	Cancer (0.316) Cell Proliferation (0.316) Inflammation (0.316)	pINCY
183	2947188	Nervous (0.308) Gastrointestinal (0.154) Reproductive (0.154)	Cancer (0.346) Inflammation (0.308) Cell Proliferation (0.154) Trauma (0.154)	pINCY
184	3094001	Reproductive (0.266) Gastrointestinal (0.160) Nervous (0.160)	Cancer (0.500) Inflammation (0.223) Cell Proliferation (0.160)	pINCY
185	3110061	Cardiovascular (0.333) Hematopoietic/Immune (0.267) Nervous (0.200) Reproductive (0.200)	Inflammation (0.467) Cancer (0.400) Cell Proliferation (0.267)	pINCY
186	3146614	Reproductive (0.326) Nervous (0.209) Gastrointestinal (0.163)	Cancer (0.512) Inflammation (0.186)	pINCY
187	3295381	Hematopoietic/Immune (0.267) Musculoskeletal (0.200) Reproductive (0.200)	Cancer (0.533) Inflammation (0.400)	pINCY
188	3364774	Nervous (0.375) Gastrointestinal (0.208) Reproductive (0.167)	Cancer (0.583) Cell Proliferation (0.250)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
189	3397777 Reproductive (0.231) Cardiovascular (0.154) Gastrointestinal (0.154) Endocrine (0.154) Hematopoietic/Immune (0.154)	Cancer (0.462) Inflammation (0.385)	pINCY
190	3403046 Reproductive (0.500) Hematopoietic/Immune (0.250) Nervous (0.250)	Cancer (0.500) Inflammation (0.250)	pINCY
191	3538506 Reproductive (0.438) Gastrointestinal (0.188) Hematopoietic/Immune (0.188) Nervous (0.188)	Cancer (0.625) Trauma (0.250) Cell Proliferation (0.188)	pINCY
192	3575519 Cardiovascular (0.455) Musculoskeletal (0.273)	Trauma (0.455) Cancer (0.273)	pINCY
193	3598694 Nervous (0.247) Reproductive (0.247)	Cancer (0.575) Cell Proliferation (0.233) Inflammation (0.110)	pINCY
194	3638819 Reproductive (0.333) Nervous (0.222) Gastrointestinal (0.111)	Cancer (0.556) Inflammation (0.185)	pINCY
195	3717139 Hematopoietic/Immune (0.500) Reproductive (0.500)	Cancer (0.500) Inflammation (0.500)	pINCY
196	3892962 Reproductive (0.455) Musculoskeletal (0.182) Nervous (0.182)	Cancer (0.909) Cell Proliferation (0.182)	pINCY
197	4153521 Nervous (0.281) Urologic (0.156) Reproductive (0.141)	Cancer (0.453) Inflammation (0.203) Cell Proliferation (0.156)	pINCY
198	4585038 Cardiovascular (0.261) Nervous (0.261) Hematopoietic/Immune (0.174)	Cancer (0.261) Inflammation (0.261) Cell Proliferation (0.130) Trauma (0.130)	pINCY
199	4674640 Nervous (0.283) Reproductive (0.239) Gastrointestinal (0.174)	Cancer (0.391) Inflammation (0.304) Cell Proliferation (0.109) Neurological (0.109)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
200	4676066 Reproductive (0.317) Cardiovascular (0.175) Gastrointestinal (0.175) Nervous (0.175)	Cancer (0.508) Inflammation (0.159) Trauma (0.127)	pINCY
201	4830687 Reproductive (0.276) Gastrointestinal (0.147) Nervous (0.147)	Cancer (0.482) Cell Proliferation (0.218) Inflammation (0.194)	pINCY
202	4880891 Hematopoietic/Immune (0.190) Gastrointestinal (0.159) Nervous (0.159)	Cancer (0.381) Inflammation (0.333) Cell Proliferation (0.222)	pINCY
203	4909754 Reproductive (0.333) Hematopoietic/Immune (0.190) Gastrointestinal (0.143)	Cancer (0.381) Inflammation (0.333) Cell Proliferation (0.286)	pINCY
204	4911931 Nervous (0.219) Hematopoietic/Immune (0.188) Reproductive (0.125) Cardiovascular (0.125)	Cancer (0.375) Cell Proliferation (0.312) Inflammation (0.219)	pINCY
205	4920433 Reproductive (1.000)	Inflammation (1.000)	pINCY
206	5042113 Gastrointestinal (0.206) Reproductive (0.159) Nervous (0.159)	Cancer (0.413) Inflammation (0.206) Cell Proliferation (0.190)	pINCY
207	5083853 Gastrointestinal (0.250) Hematopoietic/Immune (0.250) Musculoskeletal (0.125) Reproductive (0.125) Cardiovascular (0.125) Nervous (0.125)	Cancer (0.375) Inflammation (0.375) Neurological (0.125)	pINCY
208	5283981 Reproductive (0.686)	Cancer (0.514) Inflammation (0.171) Cell Proliferation (0.114)	pINCY
209	5510549 Hematopoietic/Immune (0.222) Reproductive (0.222) Nervous (0.148)	Cancer (0.593) Inflammation (0.148) Trauma (0.111) Cell Proliferation (0.111)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
210	5544862	Trauma (0.333) Inflammation (0.222) Cell Proliferation (0.111) Neurological (0.111) Cancer (0.111)	pINCY
211	5573394	Cancer (0.463) Inflammation (0.343) Cell Proliferation (0.164)	pINCY
212	5850840	Cancer (0.416) Inflammation (0.208) Cell Proliferation (0.134)	pINCY
213	5942936	Cancer (0.556) Inflammation (0.333) Neurological (0.111) Trauma (0.111)	pINCY
214	5951431	Cancer (0.518) Inflammation (0.194) Cell Proliferation (0.180)	pINCY

Table 4

Nucleotide SEQ ID NO:	Library	Library Description
108 095210	PITUNOT01	Library was constructed using RNA isolated from pituitary glands removed from a pool of 18 male and female Caucasian donors, 16 to 70 years old, who died from trauma. (RNA came from Clontech.)
109 157953	THP1PLB02	Library was constructed by reamplification of a library made using RNA isolated from THP-1 cells cultured for 48 hours with 100 ng/ml phorbol ester (PMA), followed by a 4-hour culture in media containing 1 ug/ml LPS. THP-1 is a human promonocyte line derived from the peripheral blood of a 1-year-old male with acute monocytic leukemia. One million primary clones were amplified following phage packaging.
110 159196	ADENINB01	Library was constructed using RNA isolated from the inflamed adenoid tissue of a 3-year-old child. (RNA came from Clontech.)
111 343338	THYMNOT02	Library was constructed using RNA isolated from thymus tissue removed from a 3-year-old Caucasian male, who died from drowning.
112 402386	TMLR3DT01	Library was constructed using RNA isolated from non-adherent and adherent peripheral blood mononuclear cells collected from two unrelated Caucasian male donors (25 and 29 years old).
113 456487	KERANOT01	Library was constructed using RNA isolated from neonatal keratinocytes obtained from the leg skin of a spontaneously aborted black male.
114 490256	HNT2AGT01	Library was constructed at Stratagene (STR937233), using RNA isolated from the hNT2 cell line derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor. Cells were treated with retinoic acid for 5 weeks, with mitotic inhibitors for two weeks and allowed to mature for an additional 4 weeks in conditioned medium.
115 494740	HNT2NOT01	Library was constructed at Stratagene (STR937230), using RNA isolated from the hNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor).
116 507475	TMLR3DT01	Library was constructed using RNA isolated from non-adherent and adherent peripheral blood mononuclear cells collected from two unrelated Caucasian male donors (25 and 29 years old).
117 531581	BRAINOT03	Library was constructed using RNA isolated from brain tissue removed from a 26-year-old Caucasian male during cranioplasty and excision of a cerebral meningeal lesion. Pathology for the associated tumor tissue indicated a grade 4 oligoastrocytoma in the right fronto-parietal part of the brain.
118 675190	CRBLNOT01	Library was constructed using RNA isolated from the cerebellum tissue of a 69-year-old Caucasian male who died from chronic obstructive pulmonary disease. Patient history included myocardial infarction, hypertension, and osteoarthritis.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
119 685434	UTRSNOT02	Library was constructed using RNA isolated from uterine tissue removed from a 34-year-old Caucasian female during a vaginal hysterectomy. Patient history included mitral valve disorder. Family history included stomach cancer, congenital heart anomaly, irritable bowel syndrome, ulcerative colitis, colon cancer, cerebrovascular disease, type II diabetes, and depression.
120 788663	PROSNOT05	Library was constructed using RNA isolated from diseased prostate tissue removed from a 67-year-old Caucasian male during radical prostatectomy and lymph node biopsy. This library has been determined to contain some tumor cells. Pathology indicated adenofibromatous hyperplasia was present. Pathology for the associated tumor tissue indicated adenocarcinoma Gleason grade 3+3. Patient history included coronary artery disease, stomach ulcer, and osteoarthritis. Family history included congestive heart failure.
121 870100	LUNGAST01	Library was constructed using RNA isolated from the lung tissue of a 17-year-old Caucasian male, who died from head trauma. Patient history included asthma.
122 879500	THYRNOT02	Library was constructed using RNA isolated from the diseased thyroid tissue of a 16-year-old Caucasian female with Graves' disease (hyperthyroidism).
123 975377	MUSCNOT02	Library was constructed using RNA isolated from the psoas muscle tissue of a 12-year-old Caucasian male.
124 1208721	BRSTNOT02	Library was constructed using RNA isolated from diseased breast tissue removed from a 55-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated proliferative fibrocystic changes characterized by apocrine metaplasia, sclerosing adenosis, cyst formation, and ductal hyperplasia without atypia. Pathology for the associated tumor tissue indicated an invasive grade 4 mammary adenocarcinoma. Patient history included atrial tachycardia and a benign neoplasm. Family history included cardiovascular and cerebrovascular disease.
125 1234329	LUNGFET03	Library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation.
126 1238747	LUNGUT02	Library was constructed using RNA isolated from the metastatic lung tumor tissue of a 79-year-old Caucasian male. Pathology indicated a grade 4 carcinoma of the upper and lower left lobes. Patient history included a benign prostate neoplasm, atherosclerosis, and tobacco use.
127 1265980	BRAINOT09	Library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus, who died at 23 weeks' gestation.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
128 1297333	BRSTNOT07	Library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocytic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.
129 1312824	BLADTUT02	Library was constructed using RNA isolated from bladder tumor tissue removed from an 80-year-old Caucasian female during a radical cystectomy and lymph node excision. Pathology indicated grade 3 invasive transitional cell carcinoma. Family history included acute renal failure, osteoarthritis, and atherosclerosis.
130 1359294	LUNGNOT12	Library was constructed using RNA isolated from lung tissue removed from a 78-year-old Caucasian male during a segmental lung resection and regional lymph node resection. Pathology indicated fibrosis pleura was puckered, but not invaded. Pathology for the associated tumor tissue indicated an invasive pulmonary grade 3 adenocarcinoma. Patient history included cerebrovascular disease, arteriosclerotic coronary artery disease, thrombophlebitis, chronic obstructive pulmonary disease, and asthma. Family history included intracranial hematoma, cerebrovascular disease, arteriosclerotic coronary artery disease, and type I diabetes.
131 1377380	LUNGNOT10	Library was constructed using RNA isolated from the lung tissue of a Caucasian male fetus, who died at 23 weeks' gestation.
132 1383473	BRAITUT08	Library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 47-year-old Caucasian male during excision of cerebral meningeal tissue. Pathology indicated grade 4 fibrillary astrocytoma with focal tumoral radionecrosis. Patient history included cerebrovascular disease, deficiency anemia, hyperlipidemia, epilepsy, and tobacco use. Family history included cerebrovascular disease and a malignant prostate neoplasm.
133 1388860	EOSINOT01	Library was constructed using RNA isolated from microscopically normal eosinophils from 31 non-allergic donors.
134 1395322	THYRNOT03	Library was constructed using RNA isolated from thyroid tissue removed from the left thyroid of a 28-year-old Caucasian female during a complete thyroidectomy. Pathology indicated a small nodule of adenomatous hyperplasia present in the left thyroid. Pathology for the associated tumor tissue indicated dominant follicular adenoma, forming a well-encapsulated mass in the left thyroid.
135 1419370	KIDNNOT09	Library was constructed using RNA isolated from the kidney tissue of a Caucasian male fetus, who died at 23 weeks' gestation.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
136 1429773	SINTBST01	Library was constructed using RNA isolated from ileum tissue obtained from an 18-year-old Caucasian female during bowel anastomosis. Pathology indicated Crohn's disease of the ileum, involving 15 cm of the small bowel. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.
137 1470820	PANCTUT02	Library was constructed using RNA isolated from pancreatic tumor tissue removed from a 45-year-old Caucasian female during radical pancreaticoduodenectomy. Pathology indicated a grade 4 anaplastic carcinoma. Family history included benign hypertension, hyperlipidemia and atherosclerotic coronary artery disease.
138 1483455	CORPNOT02	Library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.
139 1527064	UCMCL5T01	Library was constructed using RNA isolated from mononuclear cells obtained from the umbilical cord blood of 12 individuals. The cells were cultured for 12 days with IL-5 before RNA was obtained from the pooled lysates.
140 1557491	BLADTUT04	Library was constructed using RNA isolated from bladder tumor tissue removed from a 60-year-old Caucasian male during a radical cystectomy, prostatectomy, and vasectomy. Pathology indicated grade 3 transitional cell carcinoma in the left bladder wall. Carcinoma in-situ was identified in the dome and trigone. Patient history included tobacco use. Family history included type I diabetes, malignant neoplasm of the stomach, atherosclerotic coronary artery disease, and acute myocardial infarction.
141 1576862	LNODNOT03	Library was constructed using RNA isolated from lymph node tissue obtained from a 67-year-old Caucasian male during a segmental lung resection and bronchoscopy. This tissue was extensively necrotic with 10% viable tumor. Pathology for the associated tumor tissue indicated invasive grade 3-4 squamous cell carcinoma. Patient history included hemangioma. Family history included atherosclerotic coronary artery disease, benign hypertension, and congestive heart failure.
142 1609731	COLNTUT06	Library was constructed using RNA isolated from colon tumor tissue obtained from a 45-year-old Caucasian female during a total colectomy and total abdominal hysterectomy. Pathology indicated invasive grade 2 colonic adenocarcinoma forming a cecal mass. Patient history included benign neoplasms of the rectum and anus, multiple sclerosis and mitral valve disorder. Previous surgeries included a polypectomy. Family history included type I diabetes, cerebrovascular disease, malignant skin neoplasm, hypertension, atherosclerotic coronary artery disease and malignant neoplasm of the colon.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
143 1674538	BLADNOT05	Library was constructed using RNA isolated from bladder tissue removed from a 60-year-old Caucasian male during a radical cystectomy, prostatectomy, and vasectomy. Pathology for the associated tumor tissue indicated grade 3 transitional cell carcinoma. Carcinoma in-situ was identified in the dome and trigone. Patient history included tobacco use.
144 1675287	BLADNOT05	Library was constructed using RNA isolated from bladder tissue removed from a 60-year-old Caucasian male during a radical cystectomy, prostatectomy, and vasectomy. Pathology for the associated tumor tissue indicated grade 3 transitional cell carcinoma. Carcinoma in-situ was identified in the dome and trigone. Patient history included tobacco use.
145 1693903	COLNNOT23	Library was constructed using RNA isolated from diseased colon tissue removed from a 16-year-old Caucasian male during a total colectomy with abdominal/perineal resection. Pathology indicated gastritis and pancolitis consistent with the acute phase of ulcerative colitis. Inflammation was more severe in the transverse colon, with inflammation confined to the mucosa. There was only mild involvement of the ascending and sigmoid colon. Family history included irritable bowel syndrome.
146 1702962	DUODNOT02	Library was constructed using RNA isolated from duodenal tissue of an 8-year-old Caucasian female, who died from head trauma. Serology was positive for cytomegalovirus (CMV).
147 1712916	PROSNOT16	Library was constructed using RNA isolated from diseased prostate tissue removed from a 68-year-old Caucasian male during a radical prostatectomy. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma (Gleason grade 3+4). The patient presented with elevated prostate specific antigen (PSA). During this hospitalization, the patient was diagnosed with myasthenia gravis. Patient history included osteoarthritis, and type II diabetes. Family history included benign hypertension, acute myocardial infarction, hyperlipidemia, and arteriosclerotic coronary artery disease.
148 1748313	STOMTUT02	Library was constructed using RNA isolated from stomach tumor tissue obtained from a 68-year-old Caucasian female during a partial gastrectomy. Pathology indicated a malignant lymphoma of diffuse large-cell type. Previous surgeries included cholecystectomy. Patient history included thalassemia. Family history included acute leukemia, malignant esophagus and stomach neoplasms, and atherosclerotic coronary artery disease.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
149 1754833	LIVRUT01	Library was constructed using RNA isolated from liver tumor tissue removed from a 51-year-old Caucasian female during a hepatic lobectomy. Pathology indicated metastatic grade 3 adenocarcinoma consistent with colon cancer. Family history included a malignant neoplasm of the liver.
150 1798701	COLNNOT27	Library was constructed using RNA isolated from diseased cecal tissue removed from a 31-year-old Caucasian male during a total intra-abdominal colectomy, appendectomy, and permanent ileostomy. Pathology indicated severe active Crohn's disease involving the colon from the cecum to the rectum. There were deep rake-like ulcerations that spared the intervening mucosa. The ulcers extended into the muscularis, and there was transmural inflammation. Patient history included an irritable colon. Previous surgeries included a colonoscopy.
151 1842496	COLNNOT07	Library was constructed using RNA isolated from colon tissue removed from a 60-year-old Caucasian male during a left hemicolectomy.
152 1868613	SKINBIT01	Library was constructed using RNA isolated from diseased skin tissue of the left lower leg. Patient history included erythema nodosum of the left lower leg.
153 1870609	SKINBIT01	Library was constructed using RNA isolated from diseased skin tissue of the left lower leg. Patient history included erythema nodosum of the left lower leg.
154 1871961	LEUKNOT02	Library was constructed using RNA isolated from white blood cells of a 45-year-old female with blood type O+. The donor tested positive for cytomegalovirus (CMV).
155 1876258	LEUKNOT02	Library was constructed using RNA isolated from white blood cells of a 45-year-old female with blood type O+. The donor tested positive for cytomegalovirus (CMV).
156 1929822	COLNTUT03	Library was constructed using RNA isolated from colon tumor tissue obtained from the sigmoid colon of a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy. Pathology indicated invasive grade 2 adenocarcinoma. One lymph node contained metastasis with extranodal extension. Patient history included hyperlipidemia, cataract disorder, and dermatitis. Family history included benign hypertension, atherosclerotic coronary artery disease, hyperlipidemia, breast cancer and prostate cancer.
157 1970095	UCMCL5T01	Library was constructed using RNA isolated from mononuclear cells obtained from the umbilical cord blood of 12 individuals. The cells were cultured for 12 days with IL-5 before RNA was obtained from the pooled lysates.
158 1975473	PANCTUT02	Library was constructed using RNA isolated from pancreatic tumor tissue removed from a 45-year-old Caucasian female during radical pancreaticoduodenectomy. Pathology indicated a grade 4 anaplastic carcinoma. Family history included benign hypertension, hyperlipidemia and atherosclerotic coronary artery disease.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
159	1976527 PANCYTUT02	Library was constructed using RNA isolated from pancreatic tumor tissue removed from a 45-year-old Caucasian female during radical pancreaticoduodenectomy. Pathology indicated a grade 4 anaplastic carcinoma. Family history included benign hypertension, hyperlipidemia and atherosclerotic coronary artery disease.
160	2108023 BRAITUT03	Library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 17-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a grade 4 fibrillary giant and small-cell astrocytoma. Family history included benign hypertension and cerebrovascular disease.
161	2135746 ENDCNOT01	Library was constructed using RNA isolated from endothelial cells removed from the coronary artery of a 58-year-old Hispanic male.
162	2154810 BRAINTOT09	Library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus, who died at 23 weeks' gestation.
163	2228991 PROSNOT16	Library was constructed using RNA isolated from diseased prostate tissue removed from a 68-year-old Caucasian male during a radical prostatectomy. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma (Gleason grade 3+4). The patient presented with elevated prostate specific antigen (PSA). During this hospitalization, the patient was diagnosed with myasthenia gravis. Patient history included osteoarthritis, and type II diabetes. Family history included benign hypertension, acute myocardial infarction, hyperlipidemia, and arteriosclerotic coronary artery disease.
164	2241206 PANCYTUT02	Library was constructed using RNA isolated from pancreatic tumor tissue removed from a 45-year-old Caucasian female during radical pancreaticoduodenectomy. Pathology indicated a grade 4 anaplastic carcinoma. Family history included benign hypertension, hyperlipidemia and atherosclerotic coronary artery disease.
165	2259590 OVARTUT01	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology indicated grade 2 mucinous cystadenocarcinoma involving the entire left ovary. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.
166	2307537 NGANNOT01	Library was constructed using RNA isolated from tumorous neuroganglion tissue removed from a 9-year-old Caucasian male during a soft tissue excision of the chest wall. Pathology indicated a ganglioneuroma. Family history included asthma.
167	2440675 EOSITXT01	Library was constructed using RNA isolated from eosinophils stimulated with IL-5.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
168 2463542	THYRN0T03	Library was constructed isolated from the diseased left thyroid tissue removed from a 13-year-old Caucasian female during a complete thyroidectomy. Pathology indicated lymphocytic thyroiditis.
169 2486031	CONUTUT01	Library was constructed using RNA isolated from sigmoid mesentery tumor tissue obtained from a 61-year-old female during a total abdominal hysterectomy and bilateral salpingo-oophorectomy with regional lymph node excision. Pathology indicated a metastatic grade 4 malignant mixed müllerian tumor present in the sigmoid mesentery at two sites.
170 2493052	ADRETUT05	Library was constructed using RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.
171 2512074	CONUTUT01	Library was constructed using RNA isolated from sigmoid mesentery tumor tissue obtained from a 61-year-old female during a total abdominal hysterectomy and bilateral salpingo-oophorectomy with regional lymph node excision. Pathology indicated a metastatic grade 4 malignant mixed müllerian tumor present in the sigmoid mesentery at two sites.
172 2646274	LUNGUTUT11	Library was constructed using RNA isolated from lung tumor tissue removed from the right lower lobe of a 57-year-old Caucasian male during a segmental lung resection. Pathology indicated an infiltrating grade 4 squamous cell carcinoma. Multiple intrapulmonary peribronchial lymph nodes showed metastatic squamous cell carcinoma. Patient history included a benign brain neoplasm and tobacco abuse. Family history included spinal cord cancer, type II diabetes, cerebrovascular disease, and malignant prostate neoplasm.
173 2672566	KIDNNOT19	Library was constructed using RNA isolated from kidney tissue removed a 65-year-old Caucasian male during an exploratory laparotomy and nephroureterectomy. Patient history included malignant melanoma of the abdominal skin, benign neoplasm of colon, cerebrovascular disease, and umbilical hernia. Family history included cerebrovascular disease, prostate cancer, myocardial infarction, and atherosclerotic coronary artery disease.
174 2689674	LUNGNOT23	Library was constructed using RNA isolated from left lobe lung tissue removed from a 58-year-old Caucasian male. Patient history included soft tissue cancer, secondary cancer of the lung, prostate cancer, and an acute duodenal ulcer with hemorrhage. Family history included prostate cancer, breast cancer, and acute leukemia.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
175 2703282	OVRTUT10	Library was constructed using RNA isolated from ovarian tumor tissue removed from the left ovary of a 58-year-old Caucasian female during a total abdominal hysterectomy, removal of a solitary ovary, and repair of inguinal hernia. Pathology indicated a metastatic grade 3 adenocarcinoma of colonic origin, forming a partially cystic and necrotic tumor mass in the left ovary, and an adenocarcinoma of colonic origin, forming a nodule in the left mesovarium. A single intramural leiomyoma was identified in the myometrium. The cervix showed mild chronic cystic cervicitis. Patient history included benign hypertension, follicular cyst of the ovary, colon cancer, benign colon neoplasm, and osteoarthritis. Family history included emphysema, myocardial infarction, atherosclerotic coronary artery disease, benign hypertension, and hyperlipidemia.
176 2738293	OVARNOT09	Library was constructed using RNA isolated from ovarian tissue removed from a 28-year-old Caucasian female during a vaginal hysterectomy and removal of the fallopian tubes and ovaries. Pathology indicated multiple follicular cysts ranging in size from 0.4 to 1.5 cm in the right and left ovaries, chronic cervicitis and squamous metaplasia of the cervix, and endometrium in weakly proliferative phase. Family history included benign hypertension, hyperlipidemia, and atherosclerotic coronary artery disease.
177 2772776	PANCNOT15	Library was constructed using RNA isolated from diseased pancreatic tissue removed from a 15-year-old Caucasian male during an exploratory laparotomy with distal pancreatectomy and total splenectomy. Pathology indicated islet cell hyperplasia. Family history included prostate cancer and cardiovascular disease.
178 2774476	PANCNOT15	Library was constructed using RNA isolated from diseased pancreatic tissue removed from a 15-year-old Caucasian male during an exploratory laparotomy with distal pancreatectomy and total splenectomy. Pathology indicated islet cell hyperplasia. Family history included prostate cancer and cardiovascular disease.
179 2804624	BLADTUT08	Library was constructed using RNA isolated from bladder tumor tissue removed from a 72-year-old Caucasian male during a radical cystectomy and prostatectomy. Pathology indicated an invasive grade 3 (of 3) transitional cell carcinoma in the right bladder base. Patient history included pure hypercholesterolemia and tobacco abuse. Family history included cerebrovascular disease, brain cancer, and myocardial infarction.
180 2848225	BRSTTUT13	Library was constructed using RNA isolated from breast tumor tissue removed from the right breast of a 46-year-old Caucasian female during a unilateral extended simple mastectomy with breast reconstruction. Pathology indicated an invasive grade 3 adenocarcinoma, ductal type with apocrine features and greater than 50% intraductal component. Patient history included breast cancer.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
181 2882241	UTRSTUT05	Library was constructed using RNA isolated from uterine tumor tissue removed from a 41-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. Pathology indicated uterine leiomyoma. The endometrium was secretory and contained fragments of endometrial polyps. Benign endo- and ectocervical mucosa were identified in the endocervix. Patient history included a ventral hernia and a benign ovarian neoplasm.
182 2939011	THYMFET02	Library was constructed using RNA isolated from thymus tissue removed from a Caucasian female fetus, who died at 17 weeks' gestation from anencephalus.
183 2947188	BRAITUT23	Library was constructed using RNA isolated from left posterior brain tumor tissue removed from a 36-year-old male during a cerebral meninges lesion excision. Pathology indicated meningioma. Family history included malignant skin melanoma, atherosclerotic coronary artery disease, repair of unspecified vessel, hyperlipidemia, Huntington's chorea, and rheumatoid arthritis.
184 3094001	BRSTNOT19	Library was constructed using RNA isolated from breast tissue removed from a 67-year-old Caucasian female during a unilateral extended simple mastectomy. Patient history included depressive disorder and benign large bowel neoplasm. Family history included cerebrovascular disease, benign hypertension, congestive heart failure, and lung cancer.
185 3110061	BRSTNOT19	Library was constructed using RNA isolated from breast tissue removed from a 67-year-old Caucasian female during a unilateral extended simple mastectomy. Patient history included depressive disorder, benign large bowel neoplasm, and hemorrhoids. Family history included cerebrovascular and cardiovascular disease and lung cancer.
186 3146614	BRSTTUT15	Library was constructed using RNA isolated from breast tumor tissue removed from a 46-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated invasive grade 3, nuclear grade 2 adenocarcinoma, ductal type. An intraductal carcinoma component, non-comedo, comprised approximately 50% of the neoplasm, including the lactiferous ducts. Angiolymphatic involvement was present. Metastatic adenocarcinoma was present in 7 of 10 axillary lymph nodes. The largest nodal metastasis measured 3 cm, and focal extracapsular extension was identified. Family history included atherosclerotic coronary artery disease, type II diabetes, cerebrovascular disease, and depression.
187 3295381	PENCNOT06	Library was constructed using RNA isolated from penis corpora cavernosa tissue removed from a 3-year-old Black male.
188 3364774	TLXJINT01	Library was constructed using RNA isolated from a Jurkat cell line derived from the T cells of a male. The cells were treated for 18 hours with 50 ng/ml phorbol ester (PMA) and 1 micromolar calcium ionophore. Patient history included acute T-cell leukemia.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
189 3397777	PROSBPT02	Library was constructed using RNA isolated from diseased prostate tissue removed from a 65-year-old Caucasian male during a radical prostatectomy. Pathology indicated benign prostatic hyperplasia (BPH). One (of 7) right pelvic lymph nodes was positive for metastatic adenocarcinoma. The patient presented with induration and elevated prostate specific antigen (PSA). Patient history included a benign neoplasm of the large bowel and benign hypertension.
190 3403046	ESOGNOT03	Library was constructed using RNA isolated from esophageal tissue obtained from a 53-year-old Caucasian male during a partial esophagectomy, proximal gastrectomy, and regional lymph node biopsy. Patient history included membranous nephritis, hyperlipidemia, benign hypertension, and anxiety state. Previous surgeries included an adenotonsillectomy. Family history included cirrhosis, abdominal aortic aneurysm rupture, breast cancer, myocardial infarction, and atherosclerotic coronary artery disease.
191 3538506	SEMVNOT04	Library was constructed using RNA isolated from seminal vesicle tissue removed from a 61-year-old Caucasian male during a radical prostatectomy. Pathology for the associated tumor tissue indicated adenocarcinoma, Gleason grade 3+3. The patient presented with induration, hyperplasia of the prostate, and elevated prostate specific antigen. Patient history included renal failure, osteoarthritis, left renal artery stenosis, thrombocytopenia, hyperlipidemia, and hepatitis C (carrier). Family history included benign hypertension.
192 3575519	BRONNOT01	Library was constructed using RNA isolated from bronchial tissue removed from a 15-year-old Caucasian male.
193 3598694	FIBPNOT01	Library was constructed using RNA isolated from fibroblasts of the prostate stroma removed from a male fetus, who died after 26 weeks' gestation.
194 3638819	LUNGNOT30	Library was constructed using RNA isolated from lung tissue removed from a Caucasian male fetus, who died from Patau's syndrome (trisomy 13) at 20-weeks' gestation.
195 3717139	PENCNOT10	Library was constructed using RNA isolated from penis left corpora cavernosa tissue removed from a male.
196 3892962	BRSTTUT16	Library was constructed using RNA isolated from breast tumor tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated recurrent grade 4, nuclear grade 3, ductal carcinoma. Angiolymphatic space invasion was identified. Left breast needle biopsy indicated grade 4 ductal adenocarcinoma. Paraffin embedded tissue was estrogen positive. Patient history included breast cancer and deficiency anemia. Family history included cervical cancer.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
197 4153521	MUSLTWT01	Library was constructed using RNA isolated from glossal muscle tissue removed from a 41-year-old Caucasian female during partial glossectomy. Pathology for the matched tumor tissue indicated invasive grade 3, squamous cell carcinoma forming an ulcerated mass of the tongue. The tumor infiltrated superficially into muscle. One high lymph node contained a necrotizing granuloma. The patient presented with a complicated open wound of the tongue. Patient history included obesity, unspecified nasal and sinus disease, and normal delivery. Patient medications included Premarin, Hydrocodone, and Equate nasal spray. Family history included benign hypertension, atherosclerotic coronary artery disease, upper lobe lung cancer, type II diabetes, hyperlipidemia, and cirrhosis of the liver.
198 4585038	OVARNOT13	Library was constructed using RNA isolated from left ovary tissue removed from a 47-year-old Caucasian female during a vaginal hysterectomy with bilateral salpingo-oophorectomy, and dilation and curettage. Pathology for the associated tumor tissue indicated a single intramural leiomyoma. The endometrium was in the secretory phase. The patient presented with metrorrhagia. Patient history included hyperlipidemia and benign hypertension. Family history included colon cancer, benign hypertension, atherosclerotic coronary artery disease, and breast cancer.
199 4674640	NOEDIT02	Library was constructed using RNA isolated from nasal polyp tissue.
200 4676066	NOEDIT02	Library was constructed using RNA isolated from nasal polyp tissue.
201 4830687	BRAVXT03	Library was constructed using RNA isolated from treated astrocytes removed from the brain of a female fetus who died after 22 weeks' gestation. The cells were treated with tumor necrosis factor-alpha (TNF) and interleukin 1 (IL-1), 10ng/ml each for 24 hours.
202 4880891	UTRMTWT01	Library was constructed using RNA isolated from myometrial tissue removed from a 45-year-old Caucasian female during vaginal hysterectomy and bilateral salpingo-oophorectomy. Pathology for the matched tumor tissue indicated multiple (23) subserosal, intramural, and submucosal leiomyomata. The endometrium was in proliferative phase. The right ovary contained an old corpus luteum. The patient presented with stress incontinence. Patient history included normal delivery. Patient medications included Motrin, iron sulfate, Premarin, prednisone, Tylenol #3, and Colace. Family history included cerebrovascular disease, depression, and atherosclerotic coronary artery disease.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
203	4909754 THYMDIT01	Library was constructed using RNA isolated from diseased thymus tissue removed from a 16-year-old Caucasian female during a total excision of thymus and regional lymph node excision. Pathology indicated thymic follicular hyperplasia. The right lateral thymus showed reactive lymph nodes. A single reactive lymph node was also identified at the inferior thymus margin. The patient presented with myasthenia gravis, malaise, fatigue, dysphagia, severe muscle weakness, and prominent eyes. Patient history included frozen face muscles. Family history included depression, hepatitis B, myocardial infarction, atherosclerotic coronary artery disease, leukemia, multiple sclerosis, and lupus.
204	4911931 THYMDIT01	Library was constructed using RNA isolated from diseased thymus tissue removed from a 16-year-old Caucasian female during a total excision of thymus and regional lymph node excision. Pathology indicated thymic follicular hyperplasia. The right lateral thymus showed reactive lymph nodes. A single reactive lymph node was also identified at the inferior thymus margin. The patient presented with myasthenia gravis, malaise, fatigue, dysphagia, severe muscle weakness, and prominent eyes. Patient history included frozen face muscles. Family history included depression, hepatitis B, myocardial infarction, atherosclerotic coronary artery disease, leukemia, multiple sclerosis, and lupus.
205	4920433 TESTNOT11	Library was constructed using RNA isolated from testicular tissue removed from a 16-year-old Caucasian male who died from hanging.
206	5042113 COLHTUT01	Library was constructed using RNA isolated from colon tumor tissue removed from the hepatic flexure of a 55-year-old Caucasian male during right hemicolectomy, incidental appendectomy, and permanent colostomy. Pathology indicated invasive grade 3 adenocarcinoma. Patient history included benign hypertension, anxiety, abnormal blood chemistry, blepharitis, heart block, osteoporosis, acne, and hyperplasia of prostate. Family history included prostate cancer, acute myocardial infarction, stroke, and atherosclerotic coronary artery disease.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
207 5083853	LNOGTUT01	Library was constructed using RNA isolated from gastric lymph node tumor tissue removed from a 61-year-old Caucasian male during proximal gastrectomy and partial esophagectomy. Pathology indicated invasive grade 3 adenocarcinoma forming an ulcerated, plaque-like mass situated at the lower esophagus just proximal to the gastroesophageal junction, with partial involvement of cardiac mucosa. Metastatic adenocarcinoma was identified in 2 of 3 paraesophageal and 9 of 14 paraesophageal lymph nodes with perinodal extension to form grossly matted nodes. The paraesophageal lymph node contained metastatic grade 3 adenocarcinoma with perinodal extension. Tissue from the mesentery showed dense fibrosis with chronic inflammation and focal calcification. Patient history included a benign colon neoplasm and hyperlipidemia. Family history included type II diabetes, accessory sinus cancer, atherosclerotic coronary artery disease, and acute myocardial infarction.
208 5283981	TESTNON04	This normalized testis tissue library was constructed from 6.48 million independent clones from a pool of two testicular libraries. Starting RNA was made from testicular tissue removed from a 16-year-old Caucasian male who died from hanging. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al. except that a significantly longer (48-hours/round) reannealing hybridization was used.
209 5510549	BRADDIR01	Library was constructed using RNA isolated from diseased choroid plexus tissue of the lateral ventricle removed from the brain of a 57-year-old Caucasian male, who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema.
210 5544862	BRADDIR01	Library was constructed using RNA isolated from diseased choroid plexus tissue of the lateral ventricle removed from the brain of a 57-year-old Caucasian male, who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema.
211 5573394	TLYMNOT08	Library was constructed using RNA isolated from anergic allogenic T-lymphocyte tissue removed from an adult (40-50-year-old) Caucasian male. The cells were incubated for 3 days in the presence of OKT3 mAb (1 microgram/ml OKT3) and 5% human serum.
212 5850840	FIBAUNT02	Library was constructed using RNA isolated from untreated aortic adventitial fibroblasts removed from a 65-year-old Caucasian female.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Description
213 5942936	COLADIT05	Library was constructed using RNA isolated from diseased ascending colon tissue removed from a 32-year-old Caucasian male during a total intra-abdominal colectomy, abdominal-perineal rectal resection, and temporary ileostomy. Pathology indicated chronic ulcerative colitis extending in a continuous fashion from the mid-portion of the ascending colon to the rectum. This was characterized by crypt abscess formation and inflammation confined to the mucosa and submucosa. The terminal ileum exhibited ileitis and the rectal mucosa showed crypt abscess formation. The patient presented with ulcerative colitis and blood in the stools. Patient history included tobacco use. Patient medications included Imuran, prednisone, sulfasalazine, and azathioprine. Family history included ulcerative colitis, malignant breast neoplasm and acute myocardial infarction.
214 5951431	LIVRTUN04	This normalized library was constructed from 1.72 million independent clones from an untreated C3A liver tumor library. C3A is a derivative of Hep G2, a cell line derived from a hepatoblastoma removed from a 15-year-old Caucasian male. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228-9232 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48 hours/round) reannealing hybridization was used.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLJMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and, if applicable, Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	Score=10-50 bits for PFAM hits, depending on individual protein families

Table 5 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- 5 a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-107,
 b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-107,
 c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107, and
10 d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-107.

2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-107.

15

3. An isolated polynucleotide encoding a polypeptide of claim 1.

4. An isolated polynucleotide encoding a polypeptide of claim 2.

20

5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:108-214.

6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

25

7. A cell transformed with a recombinant polynucleotide of claim 6.

8. A transgenic organism comprising a recombinant polynucleotide of claim 6.

30

9. A method for producing a polypeptide of claim 1, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.

5 11. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

- a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214,
- b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:108-214,
- 10 c) a polynucleotide sequence complementary to a),
- d) a polynucleotide sequence complementary to b), and
- e) an RNA equivalent of a)-d).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a
15 polynucleotide of claim 11.

13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides
20 comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

25

14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- 30 a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

16. A composition comprising an effective amount of a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

17. A composition of claim 16, wherein the polypeptide comprises an amino acid sequence
5 selected from the group consisting of SEQ ID NO:1-107.

18. A method for treating a disease or condition associated with decreased expression of functional TRFX, comprising administering to a patient in need of such treatment the composition of claim 16.

10

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

15

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of
20 functional TRFX, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

25

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

30

24. A method for treating a disease or condition associated with overexpression of functional TRFX, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim

1, said method comprising the steps of:

a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying
5 a compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

a) combining the polypeptide of claim 1 with at least one test compound under conditions
10 permissive for the activity of the polypeptide of claim 1,

b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound,
and

c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change
15 in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method
20 comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts
25 of the compound and in the absence of the compound.

28. A method for assessing toxicity of a test compound, said method comprising:

a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at
30 least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;

c) quantifying the amount of hybridization complex; and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

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Pro	Pro	Pro	Leu	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Ala	Pro	Ser	Leu
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Pro	Leu	Ser	Leu	Pro	Ser	Phe	Asp	Leu	Pro	Gln	Pro	Pro	Val	Leu
				80					85					90
Asp	Thr	Leu	Asp	Leu	Leu	Ala	Ile	Tyr	Cys	Arg	Asn	Glu	Ala	Gly
				95					100					105
Gln	Glu	Glu	Val	Gly	Met	Pro	Pro	Leu	Pro	Pro	Pro	Gln	Gln	Pro
				110					115					120
Pro	Pro	Pro	Ser	Pro	Pro	Gln	Pro	Ser	Arg	Leu	Ala	Pro	Tyr	Pro
				125					130					135


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His Pro Ala Thr Thr Arg Gly Asp Arg Lys Gln Lys Lys Arg Asp
140 145 150
Gln Asn Lys Ser Ala Ala Leu Arg Tyr Arg Gln Arg Lys Arg Ala
155 160 165
Glu Gly Glu Ala Leu Glu Gly Glu Cys Gln Gly Leu Glu Ala Arg
170 175 180
Asn Arg Glu Leu Lys Glu Arg Ala Glu Ser Val Glu Arg Glu Ile
185 190 195
Gln Tyr Val Lys Asp Leu Leu Ile Glu Val Tyr Lys Ala Arg Ser
200 205 210
Gln Arg Thr Arg Ser Cys
215

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 <223> Incyte ID No: 159196CD1

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Glu Gly Glu Gly Gly Lys Pro Trp Arg Val Asp Asp Ser Glu Gly
20 25 30
Ser Trp Ile Pro Pro Gly Glu Lys Glu His Gly Gln Glu Ser Leu
35 40 45
Ser Asp Glu Leu Gln Glu Thr His Pro Lys Lys Pro Trp Gln Lys
50 55 60
Val Thr Val Arg Ala Arg Glu Leu Gly Asp Pro Ile Ala His Pro
65 70 75
Arg His Glu Ala Asp Glu Lys Pro Phe Ile Cys Ala Gln Cys Gly
80 85 90
Lys Thr Phe Asn Asn Thr Ser Asn Leu Arg Thr His Gln Arg Ile
95 100 105
His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Glu Cys Gly Lys Ser
110 115 120
Phe Ser Arg Ser Ser Asn Arg Ile Arg His Glu Arg Ile His Leu
125 130 135
Glu Glu Lys His Tyr Lys Cys Pro Lys Cys Gln Glu Ser Phe Arg
140 145 150
Arg Arg Ser Asp Leu Thr Thr His Gln Gln Asp His Leu Gly Lys
155 160 165
Arg Pro Tyr Arg Cys Asp Ile Cys Gly Lys Ser Phe Ser Gln Ser
170 175 180
Ala Thr Leu Ala Val His His Arg Thr His Leu Glu Pro Ala Pro
185 190 195
Tyr Ile Cys Cys Glu Cys Gly Lys Ser Phe Ser Asn Ser Ser Ser
200 205 210
Phe Gly Val His His Arg Thr His Thr Gly Glu Arg Pro Tyr Glu
215 220 225
Cys Thr Glu Cys Gly Arg Thr Phe Ser Asp Ile Ser Asn Phe Gly
230 235 240
Ala His Gln Arg Thr His Arg Gly Glu Lys Pro Tyr Arg Cys Thr
245 250 255
Val Cys Gly Lys His Phe Ser Arg Ser Ser Asn Leu Ile Arg His
260 265 270
Gln Lys Thr His Leu Gly Glu Gln Ala Gly Lys Asp Ser Ser
275 280

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<212> PRT

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<223> Incyte ID No: 343338CD1

<400> 4

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Met Ala Thr Arg Pro Ala Gly Gln Asn Leu Gln Gly Ile Glu Asp
 1          5          10          15
Lys Ile Thr Lys Met Lys Val Thr Met Val Ala Trp Asp Arg His
 20          25          30
Asp Asn Thr Val Ile Thr Ala Val Asn Asn Met Thr Leu Lys Val
 35          40          45
Trp Asn Ser Tyr Thr Gly Gln Leu Ile His Val Leu Met Gly His
 50          55          60
Glu Asp Glu Val Phe Val Leu Glu Pro His Pro Phe Asp Pro Arg
 65          70          75
Val Leu Phe Ser Ala Gly His Asp Gly Asn Val Ile Val Trp Asp
 80          85          90
Leu Ala Arg Gly Val Lys Ile Arg Ser Tyr Phe Asn Met Ile Glu
 95          100         105
Gly Gln Gly His Gly Ala Val Phe Asp Cys Lys Cys Ser Pro Asp
110         115         120
Gly Gln His Phe Ala Cys Thr Asp Ser His Gly His Leu Leu Ile
125         130         135
Phe Gly Phe Gly Ser Ser Ser Lys Tyr Asp Lys Ile Ala Asp Gln
140         145         150
Met Phe Phe His Ser Asp Tyr Arg Pro Leu Ile Arg Asp Ala Asn
155         160         165
Asn Phe Val Leu Asp Glu Gln Thr Gln Gln Ala Pro His Leu Met
170         175         180
Pro Pro Pro Phe Leu Val Asp Val Asp Gly Asn Pro His Pro Ser
185         190         195
Arg Tyr Gln Arg Leu Val Pro Gly Arg Glu Asn Cys Arg Glu Glu
200         205         210
Gln Leu Ile Pro Gln Met Gly Val Thr Ser Ser Gly Leu Asn Gln
215         220         225
Val Leu Ser Gln Gln Ala Asn Gln Glu Ile Ser Pro Leu Asp Ser
230         235         240
Met Ile Gln Arg Leu Gln Gln Glu Gln Asp Leu Arg Arg Ser Gly
245         250         255
Glu Ala Gly Ile Ser Asn Thr Ser Arg Leu Ser Arg Gly Ser Ile
260         265         270
Ser Ser Thr Ser Glu Val His Ser Pro Pro Asn Val Gly Leu Arg
275         280         285
Arg Ser Gly Gln Ile Glu Gly Val Arg Gln Met His Ser Asn Ala
290         295         300
Pro Arg Ser Glu Ile Ala Thr Glu Arg Asp Leu Val Ala Trp Ser
305         310         315
Arg Arg Val Val Val Pro Glu Leu Ser Ala Gly Val Ala Ser Arg
320         325         330
Gln Glu Glu Trp Arg Thr Ala Lys Gly Glu Glu Glu Ile Lys Thr
335         340         345
Tyr Arg Ser Glu Glu Lys Arg Lys His Leu Thr Val Pro Lys Glu
350         355         360
Asn Lys Ile Pro Thr Val Ser Lys Asn His Ala His Glu His Phe
365         370         375
Leu Asp Leu Gly Glu Ser Lys Lys Gln Gln Thr Asn Gln His Asn
380         385         390
Tyr Arg Thr Arg Ser Ala Leu Glu Glu Thr Pro Arg Pro Ser Glu
395         400         405

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Glu	Ile	Glu	Asn	Gly	Ser	Ser	Ser	Ser	Asp	Glu	Gly	Glu	Val	Val
				410					415					420
Ala	Val	Ser	Gly	Gly	Thr	Ser	Glu	Glu	Glu	Glu	Arg	Ala	Trp	His
				425					430					435
Ser	Asp	Gly	Ser	Ser	Ser	Asp	Tyr	Ser	Ser	Asp	Tyr	Ser	Asp	Trp
				440					445					450
Thr	Ala	Asp	Ala	Gly	Ile	Asn	Leu	Gln	Pro	Lys	Lys	Val	Pro	
				455					460					465
Lys	Asn	Lys	Thr	Lys	Lys	Ala	Glu	Ser	Ser	Ser	Asp	Glu	Glu	Glu
				470					475					480
Glu	Ser	Glu	Lys	Gln	Lys	Gln	Lys	Gln	Ile	Lys	Lys	Glu	Lys	Lys
				485					490					495
Lys	Val	Asn	Glu	Glu	Lys	Asp	Gly	Pro	Ile	Ser	Pro	Lys	Lys	Lys
				500					505					510
Lys	Pro	Lys	Glu	Arg	Lys	Gln	Lys	Arg	Leu	Ala	Val	Gly	Glu	Leu
				515					520					525
Thr	Glu	Asn	Gly	Leu	Thr	Leu	Glu	Glu	Trp	Leu	Pro	Ser	Thr	Trp
				530					535					540
Ile	Thr	Asp	Thr	Ile	Pro	Arg	Arg	Cys	Pro	Phe	Val	Pro	Gln	Met
				545					550					555
Gly	Asp	Glu	Val	Tyr	Tyr	Phe	Arg	Gln	Gly	His	Glu	Ala	Tyr	Val
				560					565					570
Glu	Met	Ala	Arg	Lys	Asn	Lys	Ile	Tyr	Ser	Ile	Asn	Pro	Lys	Lys
				575					580					585
Gln	Pro	Trp	His	Lys	Met	Glu	Leu	Arg	Glu	Gln	Glu	Leu	Met	Lys
				590					595					600
Ile	Val	Gly	Ile	Lys	Tyr	Glu	Val	Gly	Leu	Pro	Thr	Leu	Cys	Cys
				605					610					615
Leu	Lys	Leu	Ala	Phe	Leu	Asp	Pro	Asp	Thr	Gly	Lys	Leu	Thr	Gly
				620					625					630
Gly	Ser	Phe	Thr	Met	Lys	Tyr	His	Asp	Met	Pro	Asp	Val	Ile	Asp
				635					640					645
Phe	Leu	Val	Leu	Arg	Gln	Gln	Phe	Asp	Asp	Ala	Lys	Tyr	Arg	Arg
				650					655					660
Trp	Asn	Ile	Gly	Asp	Arg	Phe	Arg	Ser	Val	Ile	Asp	Asp	Ala	Trp
				665					670					675
Trp	Phe	Gly	Thr	Ile	Glu	Ser	Gln	Glu	Pro	Leu	Gln	Leu	Glu	Tyr
				680					685					690
Pro	Asp	Ser	Leu	Phe	Gln	Cys	Tyr	Asn	Val	Cys	Trp	Asp	Asn	Gly
				695					700					705
Asp	Thr	Glu	Lys	Val	Ser	Pro	Trp	Asp	Met	Glu	Leu	Ile	Pro	Asn
				710					715					720
Asn	Ala	Val	Phe	Pro	Glu	Glu	Leu	Gly	Thr	Ser	Val	Pro	Leu	Thr
				725					730					735
Asp	Gly	Glu	Cys	Arg	Ser	Leu	Ile	Tyr	Lys	Pro	Leu	Asp	Gly	Glu
				740					745					750
Trp	Gly	Thr	Asn	Pro	Arg	Asp	Glu	Glu	Cys	Glu	Arg	Ile	Val	Ala
				755					760					765
Gly	Ile	Asn	Gln	Leu	Met	Thr	Leu	Asp	Ile	Ala	Ser	Ala	Phe	Val
				770					775					780
Ala	Pro	Val	Asp	Leu	Gln	Ala	Tyr	Pro	Met	Tyr	Cys	Thr	Val	Val
				785					790					795
Ala	Tyr	Pro	Thr	Asp	Leu	Ser	Thr	Ile	Lys	Gln	Arg	Leu	Glu	Asn
				800					805					810
Arg	Phe	Tyr	Arg	Arg	Val	Ser	Ser	Leu	Met	Trp	Glu	Val	Arg	Tyr
				815					820					825
Ile	Glu	His	Asn	Thr	Arg	Thr	Phe	Asn	Glu	Pro	Gly	Ser	Pro	Ile
				830					835					840
Val	Lys	Ser	Ala	Lys	Phe	Val	Thr	Asp	Leu	Leu	Leu	His	Phe	Ile
				845					850					855
Lys	Asp	Gln	Thr	Cys	Tyr	Asn	Ile	Ile	Pro	Leu	Tyr	Asn	Ser	Met
				860					865					870
Lys	Lys	Lys	Val	Leu	Ser	Asp	Ser	Glu	Asp	Glu	Glu	Lys	Asp	Ala

Asn Val Pro Gly Thr Ser Thr Arg Lys	875	Arg Lys Asp His Gln Pro	880	885
	890		895	900
Arg Arg Arg Leu Arg Asn Arg Ala Gln Ser Tyr Asp Ile Gln Ala	905		910	915
Trp Lys Lys Gln Cys Glu Glu Leu Leu Asn Leu Ile Phe Gln Cys	920		925	930
Glu Asp Ser Glu Pro Phe Arg Gln Pro Val Asp Leu Leu Glu Tyr	935		940	945
Pro Asp Tyr Arg Asp Ile Ile Asp Thr Pro Met Asp Phe Ala Thr	950		955	960
Val Arg Glu Thr Leu Glu Ala Gly Asn Tyr Glu Ser Pro Met Glu	965		970	975
Leu Cys Lys Asp Val Arg Leu Ile Phe Ser Asn Ser Lys Ala Tyr	980		985	990
Thr Pro Ser Lys Arg Ser Arg Ile Tyr Ser Met Ser Leu Arg Leu	995		1000	1005
Ser Ala Phe Phe Glu His Ile Ser Ser Val Leu Ser Asp Tyr	1010		1015	1020
Lys Ser Ala Leu Arg Phe His Lys Arg Asn Thr Ile Thr Lys Arg	1025		1030	1035
Arg Lys Lys Arg Asn Arg Ser Ser Ser Val Ser Ser Ser Ala Ala	1040		1045	1050
Ser Ser Pro Glu Arg Lys Lys Arg Ile Leu Lys Pro Gln Leu Lys	1055		1060	1065
Ser Glu Ser Ser Thr Ser Ala Phe Ser Thr Pro Thr Arg Ser Ile	1070		1075	1080
Pro Pro Arg His Asn Ala Ala Gln Ile Asn Gly Lys Thr Glu Ser	1085		1090	1095
Ser Ser Val Val Arg Thr Arg Ser Asn Arg Val Val Val Asp Pro	1100		1105	1110
Val Val Thr Glu Gln Pro Ser Thr Ser Ser Ala Ala Lys Thr Phe	1115		1120	1125
Ile Thr Lys Ala Asn Ala Ser Ala Ile Pro Gly Lys Thr Ile Leu	1130		1135	1140
Glu Asn Ser Val Lys His Ser Lys Ala Leu Asn Thr Leu Ser Ser	1145		1150	1155
Pro Gly Gln Ser Ser Phe Ser His Gly Thr Arg Asn Asn Ser Ala	1160		1165	1170
Lys Glu Asn Met Glu Lys Glu Lys Pro Val Lys Arg Lys Met Lys	1175		1180	1185
Ser Ser Val Leu Pro Lys Ala Ser Thr Leu Ser Lys Ser Ser Ala	1190		1195	1200
Val Ile Glu Gln Gly Asp Cys Lys Asn Asn Ala Leu Val Pro Gly	1205		1210	1215
Thr Ile Gln Val Asn Gly His Gly Gly Gln Pro Ser Lys Leu Val	1220		1225	1230
Lys Arg Gly Pro Gly Arg Lys Pro Lys Val Glu Val Asn Thr Asn	1235		1240	1245
Ser Gly Glu Ile Ile His Lys Lys Arg Gly Arg Lys Pro Lys Lys	1250		1255	1260
Leu Gln Tyr Ala Lys Pro Glu Asp Leu Glu Gln Asn Asn Val His	1265		1270	1275
Pro Ile Arg Asp Glu Val Leu Pro Ser Ser Thr Cys Asn Phe Leu	1280		1285	1290
Ser Glu Thr Asn Asn Val Lys Glu Asp Leu Leu Gln Lys Lys Asn	1295		1300	1305
Arg Gly Gly Arg Lys Pro Lys Arg Lys Met Lys Thr Gln Lys Leu	1310		1315	1320
Asp Ala Asp Leu Leu Val Pro Ala Ser Val Lys Val Leu Arg Arg	1325		1330	1335
Ser Asn Arg Lys Lys Ile Asp Asp Pro Ile Asp Glu Glu Glu Glu	1340		1345	1350

Phe Glu Glu Leu Lys Gly Ser Glu Pro His Met Arg Thr Arg Asn
 1355 1360 1365
 Gln Gly Arg Arg Thr Ala Phe Tyr Asn Glu Asp Asp Ser Glu Glu
 1370 1375 1380
 Glu Gln Arg Gln Leu Leu Phe Glu Asp Thr Ser Leu Thr Phe Gly
 1385 1390 1395
 Thr Ser Ser Arg Gly Arg Val Arg Lys Leu Thr Glu Lys Ala Lys
 1400 1405 1410
 Ala Asn Leu Ile Gly Trp
 1415

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 20 25 30
 Asp Val Thr Leu Glu Thr Phe Arg Asn Leu Ala Ser Val Gly Ile
 35 40 45
 Gln Trp Lys Asp Gln Asp Ile Glu Asn Leu Tyr Gln Asn Leu Gly
 50 55 60
 Ile Lys Leu Arg Ser Leu Val Glu Arg Leu Cys Gly Arg Lys Glu
 65 70 75
 Gly Asn Glu His Arg Glu Thr Phe Ser Gln Ile Pro Asp Cys His
 80 85 90
 Leu Asn Lys Lys Ser Gln Thr Gly Val Lys Pro Cys Lys Cys Ser
 95 100 105
 Val Cys Gly Lys Val Phe Leu Arg His Ser Phe Leu Asp Arg His
 110 115 120
 Met Arg Ala His Ala Gly His Lys Arg Ser Glu Cys Gly Gly Glu
 125 130 135
 Trp Arg Glu Thr Pro Arg Lys Gln Lys Gln His Gly Lys Ala Ser
 140 145 150
 Ile Ser Pro Ser Ser Gly Ala Arg Arg Thr Val Thr Pro Thr Arg
 155 160 165
 Lys Arg Pro Tyr Glu Cys Lys Val Cys Gly Lys Ala Phe Asn Ser
 170 175 180
 Pro Asn Leu Phe Gln Ile His Gln Arg Thr His Thr Gly Lys Arg
 185 190 195
 Ser Tyr Lys Cys Arg Glu Ile Val Arg Ala Phe Thr Val Ser Ser
 200 205 210
 Phe Phe Arg Lys His Gly Lys Met His Thr Gly Glu Lys Arg Tyr
 215 220 225
 Glu Cys Lys Tyr Cys Gly Lys Pro Ile Asp Tyr Pro Ser Leu Phe
 230 235 240
 Gln Ile His Val Arg Thr His Ala Gly Glu Lys Pro Tyr Lys Cys
 245 250 255
 Lys Gln Cys Gly Lys Ala Phe Ile Ser Ala Gly Tyr Leu Arg Thr
 260 265 270
 His Glu Ile Arg Ser His Ala Leu Glu Lys Ser His Gln Cys Gln
 275 280 285
 Glu Cys Gly Lys Lys Leu Ser Cys Ser Ser Ser Leu His Arg His
 290 295 300
 Glu Arg Thr His Ser Gly Gly Lys Leu Tyr Glu Cys Gln Lys Cys
 305 310 315

Ala	Lys	Val	Phe	Arg	Cys	Pro	Thr	Ser	Leu	Gln	Ala	His	Glu	Arg	
				320					325					330	
Ala	His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Asn	Lys	Cys	Gly	Lys	
				335					340					345	
Thr	Phe	Asn	Tyr	Pro	Ser	Cys	Phe	Arg	Arg	His	Lys	Lys	Thr	His	
				350					355					360	
Ser	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Thr	Arg	Cys	Gly	Lys	Ala	Phe	
				365					370					375	
Gly	Trp	Cys	Ser	Ser	Leu	Arg	Arg	His	Glu	Met	Thr	His	Thr	Gly	
				380					385					390	
Glu	Lys	Pro	Phe	Asp	Cys	Lys	Gln	Cys	Gly	Lys	Val	Phe	Thr	Phe	
				395					400					405	
Ser	Asn	Tyr	Leu	Ser	Leu	Leu	Gln	Ala	Arg	Ala	Asp	Met	Pro	Gly	
				410					415					420	
Trp	Phe	Phe	Val	Phe	Trp										
				425											

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<211> 686

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 456487CD1

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Met	Gly	Asn	Ile	Leu	Thr	Cys	Arg	Val	His	Pro	Ser	Val	Ser	Leu	
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Glu	Phe	Asp	Gln	Gln	Gln	Gly	Ser	Val	Cys	Pro	Ser	Glu	Ser	Glu	
				20					25					30	
Ile	Tyr	Glu	Ala	Gly	Ala	Gly	Asp	Arg	Met	Ala	Gly	Ala	Pro	Met	
				35					40					45	
Ala	Ala	Ala	Val	Gln	Pro	Ala	Glu	Val	Thr	Val	Glu	Val	Gly	Glu	
				50					55					60	
Asp	Leu	His	Met	His	His	Val	Arg	Asp	Arg	Glu	Met	Pro	Glu	Ala	
				65					70					75	
Leu	Glu	Phe	Asn	Leu	Ser	Ala	Asn	Pro	Glu	Ala	Ser	Thr	Ile	Phe	
				80					85					90	
Gln	Arg	Asn	Ser	Gln	Thr	Asp	Ala	Leu	Glu	Phe	Asn	Pro	Ser	Ala	
				95					100					105	
Asn	Pro	Glu	Ala	Ser	Thr	Ile	Phe	Gln	Arg	Asn	Ser	Gln	Thr	Asp	
				110					115					120	
Val	Val	Glu	Ile	Arg	Arg	Ser	Asn	Cys	Thr	Asn	His	Val	Ser	Thr	
				125					130					135	
Val	Arg	Phe	Ser	Gln	Gln	Tyr	Ser	Leu	Cys	Ser	Thr	Ile	Phe	Leu	
				140					145					150	
Asp	Asp	Ser	Thr	Ala	Ile	Gln	His	Tyr	Leu	Thr	Met	Thr	Ile	Ile	
				155					160					165	
Ser	Val	Thr	Leu	Glu	Ile	Pro	His	His	Ile	Thr	Gln	Arg	Asp	Ala	
				170					175					180	
Asp	Arg	Ser	Leu	Ser	Ile	Pro	Asp	Glu	Gln	Leu	His	Ser	Phe	Ala	
				185					190					195	
Val	Ser	Thr	Val	His	Ile	Met	Lys	Lys	Arg	Asn	Gly	Gly	Gly	Ser	
				200					205					210	
Leu	Asn	Asn	Tyr	Ser	Ser	Ser	Ile	Pro	Ser	Thr	Pro	Ser	Thr	Ser	
				215					220					225	
Gln	Glu	Asp	Pro	Gln	Phe	Ser	Val	Pro	Pro	Thr	Ala	Asn	Thr	Pro	
				230					235					240	
Thr	Pro	Val	Cys	Lys	Arg	Ser	Met	Arg	Trp	Ser	Asn	Leu	Phe	Thr	
				245					250					255	
Ser	Glu	Lys	Gly	Ser	Asp	Pro	Asp	Lys	Glu	Arg	Lys	Ala	Pro	Glu	
				260					265					270	

Asn	His	Ala	Asp	Thr	Ile	Gly	Ser	Gly	Arg	Ala	Ile	Pro	Ile	Lys
				275					280					285
Gln	Gly	Met	Leu	Leu	Lys	Arg	Ser	Gly	Lys	Trp	Leu	Lys	Thr	Trp
				290					295					300
Lys	Lys	Lys	Tyr	Val	Thr	Leu	Cys	Ser	Asn	Gly	Met	Leu	Thr	Tyr
				305					310					315
Tyr	Ser	Ser	Leu	Gly	Asp	Tyr	Met	Lys	Asn	Ile	His	Lys	Lys	Glu
				320					325					330
Ile	Asp	Leu	Gln	Thr	Ser	Thr	Ile	Lys	Val	Pro	Gly	Lys	Trp	Pro
				335					340					345
Ser	Leu	Ala	Thr	Ser	Ala	Cys	Thr	Pro	Ile	Ser	Ser	Ser	Lys	Ser
				350					355					360
Asn	Gly	Leu	Ser	Lys	Asp	Met	Asp	Thr	Gly	Leu	Gly	Asp	Ser	Ile
				365					370					375
Cys	Phe	Ser	Pro	Ser	Ile	Ser	Ser	Thr	Thr	Ser	Pro	Lys	Leu	Asn
				380					385					390
Pro	Pro	Pro	Ser	Pro	His	Ala	Asn	Lys	Lys	Lys	His	Leu	Lys	Lys
				395					400					405
Lys	Ser	Thr	Asn	Asn	Phe	Met	Ile	Val	Ser	Ala	Thr	Gly	Gln	Thr
				410					415					420
Trp	His	Phe	Glu	Ala	Thr	Thr	Tyr	Glu	Glu	Arg	Asp	Ala	Trp	Val
				425					430					435
Gln	Ala	Ile	Gln	Ser	Gln	Ile	Leu	Ala	Ser	Leu	Gln	Ser	Cys	Glu
				440					445					450
Ser	Ser	Lys	Ser	Lys	Ser	Gln	Leu	Thr	Ser	Gln	Ser	Glu	Ala	Met
				455					460					465
Ala	Leu	Gln	Ser	Ile	Gln	Asn	Met	Arg	Gly	Asn	Ala	His	Cys	Val
				470					475					480
Asp	Cys	Glu	Thr	Gln	Asn	Pro	Lys	Trp	Ala	Ser	Leu	Asn	Leu	Gly
				485					490					495
Val	Leu	Met	Cys	Ile	Glu	Cys	Ser	Gly	Ile	His	Arg	Ser	Leu	Gly
				500					505					510
Thr	Arg	Leu	Ser	Arg	Val	Arg	Ser	Leu	Glu	Leu	Asp	Asp	Trp	Pro
				515					520					525
Val	Glu	Leu	Arg	Lys	Val	Met	Ser	Ser	Ile	Gly	Asn	Asp	Leu	Ala
				530					535					540
Asn	Ser	Ile	Trp	Glu	Gly	Ser	Ser	Gln	Gly	Gln	Thr	Lys	Pro	Ser
				545					550					555
Glu	Lys	Ser	Thr	Arg	Glu	Glu	Lys	Glu	Arg	Trp	Ile	Arg	Ser	Lys
				560					565					570
Tyr	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Leu	Pro	Cys	Thr	Glu	Leu
				575					580					585
Ser	Leu	Gly	Gln	Gln	Leu	Leu	Arg	Ala	Thr	Ala	Asp	Glu	Asp	Leu
				590					595					600
Gln	Thr	Ala	Ile	Leu	Leu	Leu	Ala	His	Gly	Ser	Arg	Glu	Glu	Val
				605					610					615
Asn	Glu	Thr	Cys	Gly	Glu	Gly	Asp	Gly	Cys	Thr	Ala	Leu	His	Leu
				620					625					630
Ala	Cys	Arg	Lys	Gly	Asn	Val	Val	Leu	Ala	Gln	Leu	Leu	Ile	Trp
				635					640					645
Tyr	Gly	Val	Asp	Val	Met	Ala	Arg	Asp	Ala	His	Gly	Asn	Thr	Ala
				650					655					660
Leu	Thr	Tyr	Ala	Arg	Gln	Ala	Ser	Ser	Gln	Glu	Cys	Ile	Asn	Val
				665					670					675
Leu	Leu	Gln	Tyr	Gly	Cys	Pro	Asp	Lys	Cys	Val				
				680					685					

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<211> 348

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 490256CD1

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Ile Lys Ala Glu Asp His Tyr Trp Gly Gln Asp Ser Ser Ser Gln
  20      25      30
Lys Cys Ser Pro His Arg Arg Glu Leu Tyr Arg Gln His Phe Arg
  35      40      45
Lys Leu Cys Tyr Gln Asp Ala Pro Gly Pro Arg Glu Ala Leu Thr
  50      55      60
Gln Leu Trp Glu Leu Cys Arg Gln Trp Leu Arg Pro Glu Cys His
  65      70      75
Thr Lys Glu Gln Ile Leu Asp Leu Leu Val Leu Glu Gln Ser Leu
  80      85      90
Ser Ile Leu Pro Lys Asp Leu Gln Ala Trp Val Arg Ala His His
  95     100     105
Pro Glu Thr Gly Glu Glu Ala Val Thr Val Leu Glu Asp Leu Glu
 110     115     120
Arg Glu Leu Asp Glu Pro Gly Lys Gln Val Pro Gly Asn Ser Glu
 125     130     135
Arg Arg Asp Ile Leu Met Asp Lys Leu Ala Pro Leu Gly Arg Pro
 140     145     150
Tyr Glu Ser Leu Thr Val Gln Leu His Pro Lys Lys Thr Gln Leu
 155     160     165
Glu Gln Glu Ala Gly Lys Pro Gln Arg Asn Gly Asp Lys Thr Arg
 170     175     180
Thr Lys Asn Glu Glu Leu Phe Gln Lys Glu Asp Met Pro Lys Asp
 185     190     195
Lys Glu Phe Leu Gly Glu Ile Asn Asp Arg Leu Asn Lys Asp Thr
 200     205     210
Pro Gln His Pro Lys Ser Lys Asp Ile Ile Glu Asn Glu Gly Arg
 215     220     225
Ser Glu Trp Gln Gln Arg Glu Arg Arg Arg Tyr Lys Cys Asp Glu
 230     235     240
Cys Gly Lys Ser Phe Ser His Ser Ser Asp Leu Ser Lys His Arg
 245     250     255
Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Asp Glu Cys Gly
 260     265     270
Lys Ala Phe Ile Gln Arg Ser His Leu Ile Gly His His Arg Val
 275     280     285
His Thr Gly Val Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Asp
 290     295     300
Phe Ser Gly Arg Thr Gly Leu Ile Gln His Gln Arg Ile His Thr
 305     310     315
Gly Glu Lys Pro Tyr Glu Cys Asp Glu Cys Gly Arg Pro Phe Arg
 320     325     330
Val Ser Ser Ala Leu Ile Arg His Gln Arg Ile His Thr Ala Asn
 335     340     345
Lys Leu Tyr

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<210> 8

<211> 181

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 494740CD1

<400> 8


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Met Glu Glu Ile Pro Ala Gln Glu Ala Ala Gly Ser Pro Arg Val
 1          5          10          15
Gln Phe Gln Ser Leu Glu Thr Gln Ser Glu Cys Leu Ser Pro Glu
 20          25          30
Pro Gln Phe Val Gln Asp Thr Asp Met Glu Gln Gly Leu Thr Gly
 35          40          45
Ala Pro Pro Val Pro Gln Val Pro Ala Leu Pro Arg Glu Ala Ser
 50          55          60
Pro Gly Asp Gln Ala Ala Ala Leu Leu Thr Ala Arg Tyr Gln Glu
 65          70          75
Phe Val Thr Phe Glu Asp Val Ala Val His Leu Thr Arg Glu Glu
 80          85          90
Trp Gly Tyr Leu Asp Pro Val Gln Arg Asp Leu Tyr Arg Glu Val
 95          100          105
Met Leu Glu Asn Tyr Gly Asn Val Val Ser Leu Gly Ile Leu Leu
 110          115          120
Arg Leu Pro Thr Thr Arg Ile His Ser Val Asn Ser Cys Pro Ala
 125          130          135
Leu Ser His Thr Gln Ala Ser Ala Phe Ser Gly Glu Thr Leu Ala
 140          145          150
Val Leu Thr Ala Gly Ile Ser Lys Arg Trp Pro Lys Tyr Arg Leu
 155          160          165
Pro Ile Asp Ile Ala Arg Pro Cys Ser Glu Thr Pro Phe Pro Arg
 170          175          180
Leu

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<210> 9
<211> 126
<212> PRT
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 507475CD1

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<400> 9
Met Ser Val Met Asp Leu Ala Asn Thr Cys Ser Ser Phe Gln Ser
 1          5          10          15
Asp Leu Asp Phe Cys Ser Asp Cys Gly Ser Val Leu Pro Leu Pro
 20          25          30
Gly Ala Gln Asp Thr Val Thr Cys Ile Arg Cys Gly Phe Asn Ile
 35          40          45
Asn Val Arg Asp Phe Glu Gly Lys Val Val Lys Thr Ser Val Val
 50          55          60
Phe His Gln Leu Gly Thr Ala Met Pro Met Ser Val Glu Glu Gly
 65          70          75
Pro Glu Cys Gln Gly Pro Val Val Asp Arg Arg Cys Pro Arg Cys
 80          85          90
Gly His Glu Gly Met Ala Tyr His Thr Arg Gln Met Arg Ser Ala
 95          100          105
Asp Glu Gly Gln Thr Val Phe Tyr Thr Cys Thr Asn Cys Lys Phe
 110          115          120
Gln Glu Lys Glu Asp Ser
 125

```

```

<210> 10
<211> 610
<212> PRT
<213> Homo sapiens

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<220>
<221> misc_feature

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<223> Incyte ID No: 531581CD1

<400> 10

Met	Gln	Tyr	Ser	His	His	Cys	Glu	His	Leu	Leu	Glu	Arg	Leu	Asn
1				5					10					15
Lys	Gln	Arg	Glu	Ala	Gly	Phe	Leu	Cys	Asp	Cys	Thr	Ile	Val	Ile
				20					25					30
Gly	Glu	Phe	Gln	Phe	Lys	Ala	His	Arg	Asn	Val	Leu	Ala	Ser	Phe
				35					40					45
Ser	Glu	Tyr	Phe	Gly	Ala	Ile	Tyr	Arg	Ser	Thr	Ser	Glu	Asn	Asn
				50					55					60
Val	Phe	Leu	Asp	Gln	Ser	Gln	Val	Lys	Ala	Asp	Gly	Phe	Gln	Lys
				65					70					75
Leu	Leu	Glu	Phe	Ile	Tyr	Thr	Gly	Thr	Leu	Asn	Leu	Asp	Ser	Trp
				80					85					90
Asn	Val	Lys	Glu	Ile	His	Gln	Ala	Ala	Asp	Tyr	Leu	Lys	Val	Glu
				95					100					105
Glu	Val	Val	Thr	Lys	Cys	Lys	Ile	Lys	Met	Glu	Asp	Phe	Ala	Phe
				110					115					120
Ile	Ala	Asn	Pro	Ser	Ser	Thr	Glu	Ile	Ser	Ser	Ile	Thr	Gly	Asn
				125					130					135
Ile	Glu	Leu	Asn	Gln	Gln	Thr	Cys	Leu	Leu	Thr	Leu	Arg	Asp	Tyr
				140					145					150
Asn	Asn	Arg	Glu	Lys	Ser	Glu	Val	Ser	Thr	Asp	Leu	Ile	Gln	Ala
				155					160					165
Asn	Pro	Lys	Gln	Gly	Ala	Leu	Ala	Lys	Lys	Ser	Ser	Gln	Thr	Lys
				170					175					180
Lys	Lys	Lys	Lys	Ala	Phe	Asn	Ser	Pro	Lys	Thr	Gly	Gln	Asn	Lys
				185					190					195
Thr	Val	Gln	Tyr	Pro	Ser	Asp	Ile	Leu	Glu	Asn	Ala	Ser	Val	Glu
				200					205					210
Leu	Phe	Leu	Asp	Ala	Asn	Lys	Leu	Pro	Thr	Pro	Val	Val	Glu	Gln
				215					220					225
Val	Ala	Gln	Ile	Asn	Asp	Asn	Ser	Glu	Leu	Glu	Leu	Thr	Ser	Val
				230					235					240
Val	Glu	Asn	Thr	Phe	Pro	Ala	Gln	Asp	Ile	Val	His	Thr	Val	Thr
				245					250					255
Val	Lys	Arg	Lys	Arg	Gly	Lys	Ser	Gln	Pro	Asn	Cys	Ala	Leu	Lys
				260					265					270
Glu	His	Ser	Met	Ser	Asn	Ile	Ala	Ser	Val	Lys	Ser	Pro	Tyr	Glu
				275					280					285
Ala	Glu	Asn	Ser	Gly	Glu	Glu	Leu	Asp	Gln	Arg	Tyr	Ser	Lys	Ala
				290					295					300
Lys	Pro	Met	Cys	Asn	Thr	Cys	Gly	Lys	Val	Phe	Ser	Glu	Ala	Ser
				305					310					315
Ser	Leu	Arg	Arg	His	Met	Arg	Ile	His	Lys	Gly	Val	Lys	Pro	Tyr
				320					325					330
Val	Cys	His	Leu	Cys	Gly	Lys	Ala	Phe	Thr	Gln	Cys	Asn	Gln	Leu
				335					340					345
Lys	Thr	His	Val	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys
				350					355					360
Glu	Leu	Cys	Asp	Lys	Gly	Phe	Ala	Gln	Lys	Cys	Gln	Leu	Val	Phe
				365					370					375
His	Ser	Arg	Met	His	His	Gly	Glu	Glu	Lys	Pro	Tyr	Lys	Cys	Asp
				380					385					390
Val	Cys	Asn	Leu	Gln	Phe	Ala	Thr	Ser	Ser	Asn	Leu	Lys	Ile	His
				395					400					405
Ala	Arg	Lys	His	Ser	Gly	Glu	Lys	Pro	Tyr	Val	Cys	Asp	Arg	Cys
				410					415					420
Gly	Gln	Arg	Phe	Ala	Gln	Ala	Ser	Thr	Leu	Thr	Tyr	His	Val	Arg
				425					430					435
Arg	His	Thr	Gly	Glu	Lys	Pro	Tyr	Val	Cys	Asp	Thr	Cys	Gly	Lys
				440					445					450

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<400> 12
Met Leu Tyr Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn
  1             5             10             15
His Thr Asp Glu Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala

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	20		25		30
His Gly Gln Ile Ala Val Val Glu Phe Leu Leu Gln Asn Gly Ala					
	35		40		45
Asp Pro Gln Leu Leu Gly Lys Gly Arg Glu Ser Ala Leu Ser Leu					
	50		55		60
Ala Cys Ser Lys Gly Tyr Thr Asp Ile Val Lys Met Leu Leu Asp					
	65		70		75
Cys Gly Val Asp Val Asn Glu Tyr Asp Trp Asn Gly Gly Thr Pro					
	80		85		90
Leu Leu Tyr Ala Val His Gly Asn His Val Lys Cys Val Lys Met					
	95		100		105
Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile Glu Thr Asp Ser Gly					
	110		115		120
Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Ser Val					
	125		130		135
Gln Gln Val Ile Glu Ser His Leu Leu Lys Leu Leu Gln Asn Ile					
	140		145		150
Lys Glu					

<210> 13
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 788663CD1

<400> 13	
Met Ala Asp Val Val Val Gly Lys Asp Lys Gly Gly Glu Gln Arg	
1 5 10 15	
Leu Ile Ser Leu Pro Leu Ser Arg Ile Arg Val Ile Met Lys Ser	
20 25 30	
Ser Pro Glu Val Ser Ser Ile Asn Gln Glu Ala Leu Val Leu Thr	
35 40 45	
Ala Lys Ala Thr Glu Leu Phe Val Gln Cys Leu Ala Thr Tyr Ser	
50 55 60	
Tyr Arg His Gly Ser Gly Lys Glu Lys Lys Val Leu Thr Tyr Ser	
65 70 75	
Asp Leu Ala Asn Thr Ala Gln Gln Ser Glu Thr Phe Gln Phe Leu	
80 85 90	
Ala Asp Ile Leu Pro Lys Lys Ile Leu Ala Ser Lys Tyr Leu Lys	
95 100 105	
Met Leu Lys Glu Glu Lys Arg Glu Glu Asp Glu Glu Asn Asp Asn	
110 115 120	
Asp Asn Glu Ser Asp His Asp Glu Ala Asp Ser	
125 130	

<210> 14
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 870100CD1

<400> 14	
Met Pro Arg Arg Lys Gln Ser His Pro Gln Pro Val Lys Cys Glu	
1 5 10 15	
Gly Val Lys Val Asp Thr Glu Asp Ser Leu Asp Glu Gly Pro Gly	
20 25 30	

Ala	Leu	Val	Leu	Glu	Ser	Asp	Leu	Leu	Leu	Gly	Gln	Asp	Leu	Glu
				35					40					45
Phe	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Asp	Gly	Asn	Ser	Asp
				50					55					60
Gln	Leu	Met	Gly	Phe	Glu	Arg	Asp	Ser	Glu	Gly	Asp	Ser	Leu	Gly
				65					70					75
Ala	Arg	Pro	Gly	Leu	Pro	Tyr	Gly	Leu	Ser	Asp	Asp	Glu	Ser	Gly
				80					85					90
Gly	Gly	Arg	Ala	Leu	Ser	Ala	Glu	Ser	Glu	Val	Glu	Glu	Pro	Ala
				95					100					105
Arg	Gly	Pro	Gly	Glu	Ala	Arg	Gly	Glu	Arg	Pro	Gly	Pro	Ala	Cys
				110					115					120
Gln	Leu	Cys	Gly	Gly	Pro	Thr	Gly	Glu	Gly	Pro	Cys	Cys	Gly	Ala
				125					130					135
Gly	Gly	Pro	Gly	Gly	Gly	Pro	Leu	Leu	Pro	Pro	Arg	Leu	Leu	Tyr
				140					145					150
Ser	Cys	Arg	Leu	Cys	Thr	Phe	Val	Ser	His	Tyr	Ser	Ser	His	Leu
				155					160					165
Lys	Arg	His	Met	Gln	Thr	His	Ser	Gly	Glu	Lys	Pro	Phe	Arg	Cys
				170					175					180
Gly	Arg	Cys	Pro	Tyr	Ala	Ser	Ala	Gln	Leu	Val	Asn	Leu	Thr	Arg
				185					190					195
His	Thr	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Arg	Cys	Pro	His
				200					205					210
Cys	Pro	Phe	Ala	Cys	Ser	Ser	Leu	Gly	Asn	Leu	Arg	Arg	His	Gln
				215					220					225
Arg	Thr	His	Ala	Gly	Pro	Pro	Thr	Pro	Pro	Cys	Pro	Thr	Cys	Gly
				230					235					240
Phe	Arg	Cys	Cys	Thr	Pro	Arg	Pro	Ala	Arg	Pro	Pro	Ser	Pro	Thr
				245					250					255
Glu	Gln	Glu	Gly	Ala	Val	Pro	Arg	Arg	Pro	Glu	Asp	Ala	Leu	Leu
				260					265					270
Leu	Pro	Asp	Leu	Ser	Leu	His	Val	Pro	Pro	Gly	Gly	Ala	Ser	Phe
				275					280					285
Leu	Pro	Asp	Cys	Gly	Gln	Leu	Arg	Gly	Glu	Gly	Glu	Gly	Leu	Cys
				290					295					300
Gly	Thr	Gly	Ser	Glu	Pro	Leu	Pro	Glu	Leu	Leu	Phe	Pro	Trp	Thr
				305					310					315
Cys	Arg	Gly	Cys	Gly	Gln	Glu	Leu	Glu	Glu	Gly	Glu	Gly	Ser	Arg
				320					325					330
Leu	Gly	Ala	Ala	Met	Cys	Gly	Arg	Cys	Met	Arg	Gly	Glu	Ala	Gly
				335					340					345
Gly	Gly	Ala	Ser	Gly	Gly	Pro	Gln	Gly	Pro	Ser	Asp	Lys	Gly	Phe
				350					355					360
Ala	Cys	Ser	Leu	Cys	Pro	Phe	Ala	Thr	His	Tyr	Pro	Asn	His	Leu
				365					370					375
Ala	Arg	His	Met	Lys	Thr	His	Ser	Gly	Glu	Lys	Pro	Phe	Arg	Cys
				380					385					390
Ala	Arg	Cys	Pro	Tyr	Ala	Ser	Ala	His	Leu	Asp	Asn	Leu	Lys	Arg
				395					400					405
His	Gln	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Pro	Leu
				410					415					420
Cys	Pro	Tyr	Ala	Cys	Gly	Asn	Leu	Ala	Asn	Leu	Lys	Arg	His	Gly
				425					430					435
Arg	Ile	His	Ser	Gly	Asp	Lys	Pro	Phe	Arg	Cys	Ser	Leu	Cys	Asn
				440					445					450
Tyr	Ser	Cys	Asn	Gln	Ser	Met	Asn	Leu	Lys	Arg	His	Met	Leu	Arg
				455					460					465
His	Thr	Gly	Glu	Lys	Pro	Phe	Arg	Cys	Ala	Thr	Cys	Ala	Tyr	Thr
				470					475					480
Thr	Gly	His	Trp	Asp	Asn	Tyr	Lys	Arg	His	Gln	Lys	Val	His	Gly
				485					490					495
His	Gly	Gly	Ala	Gly	Gly	Pro	Gly	Leu	Ser	Ala	Ser	Glu	Gly	Trp

	500		505		510
Ala	Pro	Pro	His	Ser	Pro
	515	Pro	Pro	Ser	Val
Pro	Ala	Leu	Gly	Thr	Ala
	530	Gly	Ser	Arg	Ala
Ser					Val
					His
					Thr
					Asp
					Ser
					540

<210> 15
 <211> 1828
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 879500CD1

<400> 15

Met	Pro	Thr	Pro	Thr	Leu	Val	Arg	Pro	Leu	Leu	Lys	Leu	Val	His
1				5					10					15
Ser	Pro	Ser	Pro	Glu	Val	Ser	Ala	Ser	Ala	Pro	Gly	Ala	Ala	Pro
				20					25					30
Leu	Thr	Ile	Ser	Ser	Pro	Leu	His	Val	Pro	Ser	Ser	Leu	Pro	Gly
				35					40					45
Pro	Ala	Ser	Ser	Pro	Met	Pro	Ile	Pro	Asn	Ser	Ser	Pro	Leu	Ala
				50					55					60
Ser	Pro	Val	Ser	Ser	Thr	Val	Ser	Val	Pro	Leu	Ser	Ser	Ser	Leu
				65					70					75
Pro	Ile	Ser	Val	Pro	Thr	Thr	Leu	Pro	Ala	Pro	Ala	Ser	Ala	Pro
				80					85					90
Leu	Thr	Ile	Pro	Ile	Ser	Ala	Pro	Leu	Thr	Val	Ser	Ala	Ser	Gly
				95					100					105
Pro	Ala	Leu	Leu	Thr	Ser	Val	Thr	Pro	Pro	Leu	Ala	Pro	Val	Val
				110					115					120
Pro	Ala	Ala	Pro	Gly	Pro	Pro	Ser	Leu	Ala	Pro	Ser	Gly	Ala	Ser
				125					130					135
Pro	Ser	Ala	Ser	Ala	Leu	Thr	Leu	Gly	Leu	Ala	Thr	Ala	Pro	Ser
				140					145					150
Leu	Ser	Ser	Ser	Gln	Thr	Pro	Gly	His	Pro	Leu	Leu	Leu	Ala	Pro
				155					160					165
Thr	Ser	Ser	His	Val	Pro	Gly	Leu	Asn	Ser	Thr	Val	Ala	Pro	Ala
				170					175					180
Cys	Ser	Pro	Val	Leu	Val	Pro	Ala	Ser	Ala	Leu	Ala	Ser	Pro	Phe
				185					190					195
Pro	Ser	Ala	Pro	Asn	Pro	Ala	Pro	Pro	Leu	Ala	Pro	Leu	Pro	Val
				200					205					210
Leu	Ala	Pro	Ser	Pro	Gly	Ala	Ala	Pro	Val	Leu	Ala	Ser	Ser	Gln
				215					220					225
Thr	Pro	Val	Pro	Val	Met	Ala	Pro	Ser	Ser	Thr	Pro	Gly	Thr	Ser
				230					235					240
Leu	Ala	Ser	Ala	Ser	Pro	Val	Pro	Ala	Pro	Thr	Pro	Val	Leu	Ala
				245					250					255
Pro	Ser	Ser	Thr	Gln	Thr	Met	Leu	Pro	Ala	Pro	Val	Pro	Ser	Pro
				260					265					270
Leu	Pro	Ser	Pro	Ala	Ser	Thr	Gln	Thr	Leu	Ala	Leu	Ala	Pro	Ala
				275					280					285
Leu	Ala	Pro	Thr	Leu	Gly	Gly	Ser	Ser	Pro	Ser	Gln	Thr	Leu	Ser
				290					295					300
Leu	Gly	Thr	Gly	Asn	Pro	Gln	Gly	Pro	Phe	Pro	Thr	Gln	Thr	Leu
				305					310					315
Ser	Leu	Thr	Pro	Ala	Ser	Ser	Leu	Val	Pro	Thr	Pro	Ala	Gln	Thr
				320					325					330
Leu	Ser	Leu	Ala	Pro	Gly	Pro	Pro	Leu	Gly	Pro	Thr	Gln	Thr	Leu

	335		340		345
Ser Leu Ala Pro	Ala	Pro Pro Leu Ala	Pro Ala Ser Pro Val	Gly	
	350		355		360
Pro Ala Pro Ala	His Thr Leu Thr Leu	Ala Pro Ala Ser Ser	Ser		
	365		370		375
Ala Ser Leu Leu	Ala Pro Ala Ser Val	Gln Thr Leu Thr Leu	Ser		
	380		385		390
Pro Ala Pro Val	Pro Thr Leu Gly Pro	Ala Ala Ala Gln Thr	Leu		
	395		400		405
Ala Leu Ala Pro	Ala Ser Thr Gln Ser	Pro Ala Ser Gln Ala	Ser		
	410		415		420
Ser Leu Val Val	Ser Ala Ser Gly Ala	Ala Pro Leu Pro Val	Thr		
	425		430		435
Met Val Ser Arg	Leu Pro Val Ser Lys	Asp Glu Pro Asp Thr	Leu		
	440		445		450
Thr Leu Arg Ser	Gly Pro Pro Ser Pro	Pro Ser Thr Ala Thr	Ser		
	455		460		465
Phe Gly Gly Pro	Arg Pro Arg Arg Gln	Pro Pro Pro Pro Pro	Arg		
	470		475		480
Ser Pro Phe Tyr	Leu Asp Ser Leu Glu	Glu Lys Arg Lys Arg	Gln		
	485		490		495
Arg Ser Glu Arg	Leu Glu Arg Ile Phe	Gln Leu Ser Glu Ala	His		
	500		505		510
Gly Ala Leu Ala	Pro Val Tyr Gly Thr	Glu Val Leu Asp Phe	Cys		
	515		520		525
Thr Leu Pro Gln	Pro Val Ala Ser Pro	Ile Gly Pro Arg Ser	Pro		
	530		535		540
Gly Pro Ser His	Pro Thr Phe Trp Thr	Tyr Thr Glu Ala Ala	His		
	545		550		555
Arg Ala Val Leu	Phe Pro Gln Gln Arg	Leu Asp Gln Leu Ser	Glu		
	560		565		570
Ile Ile Glu Arg	Phe Ile Phe Val Met	Pro Pro Val Glu Ala	Pro		
	575		580		585
Pro Pro Ser Leu	His Ala Cys His Pro	Pro Pro Trp Leu Ala	Pro		
	590		595		600
Arg Gln Ala Ala	Phe Gln Glu Gln Leu	Ala Ser Glu Leu Trp	Pro		
	605		610		615
Arg Ala Arg Pro	Leu His Arg Ile Val	Cys Asn Met Arg Thr	Gln		
	620		625		630
Phe Pro Asp Leu	Arg Leu Ile Gln Tyr	Asp Cys Gly Lys Leu	Gln		
	635		640		645
Thr Leu Ala Val	Leu Leu Arg Gln Leu	Lys Ala Glu Gly His	Arg		
	650		655		660
Val Leu Ile Phe	Thr Gln Met Thr Arg	Met Leu Asp Val Leu	Glu		
	665		670		675
Gln Phe Leu Thr	Tyr His Gly His Leu	Tyr Leu Arg Leu Asp	Gly		
	680		685		690
Ser Thr Arg Val	Glu Gln Arg Gln Ala	Leu Met Glu Arg Phe	Asn		
	695		700		705
Ala Asp Lys Arg	Ile Phe Cys Phe Ile	Leu Ser Thr Arg Ser	Gly		
	710		715		720
Gly Val Gly Val	Asn Leu Thr Gly Ala	Asp Thr Val Val Phe	Tyr		
	725		730		735
Asp Ser Asp Trp	Asn Pro Thr Met Asp	Ala Gln Ala Gln Asp	Arg		
	740		745		750
Cys His Arg Ile	Gly Gln Thr Arg Asp	Val His Ile Tyr Arg	Leu		
	755		760		765
Ile Ser Glu Arg	Thr Val Glu Glu Asn	Ile Leu Lys Lys Ala	Asn		
	770		775		780
Gln Lys Arg Met	Leu Gly Asp Met Ala	Ile Glu Gly Gly Asn	Phe		
	785		790		795
Thr Thr Ala Tyr	Phe Lys Gln Thr Ile	Arg Glu Leu Phe Asp	Met		
	800		805		810

Pro	Leu	Glu	Glu	Pro	Ser	Ser	Ser	Ser	Val	Pro	Ser	Ala	Pro	Glu
				815					820					825
Glu	Glu	Glu	Glu	Thr	Val	Ala	Ser	Lys	Gln	Thr	His	Ile	Leu	Glu
				830					835					840
Gln	Ala	Leu	Cys	Arg	Ala	Glu	Asp	Glu	Glu	Asp	Ile	Arg	Ala	Ala
				845					850					855
Thr	Gln	Ala	Lys	Ala	Glu	Gln	Val	Ala	Glu	Leu	Ala	Glu	Phe	Asn
				860					865					870
Glu	Asn	Asp	Gly	Phe	Pro	Ala	Gly	Glu	Gly	Glu	Glu	Ala	Gly	Arg
				875					880					885
Pro	Gly	Ala	Glu	Asp	Glu	Glu	Met	Ser	Arg	Ala	Glu	Gln	Glu	Ile
				890					895					900
Ala	Ala	Leu	Val	Glu	Gln	Leu	Thr	Pro	Ile	Glu	Arg	Tyr	Ala	Met
				905					910					915
Lys	Phe	Leu	Glu	Ala	Ser	Leu	Glu	Glu	Val	Ser	Arg	Glu	Glu	Leu
				920					925					930
Lys	Gln	Ala	Glu	Glu	Gln	Val	Glu	Ala	Ala	Arg	Lys	Asp	Leu	Asp
				935					940					945
Gln	Ala	Lys	Glu	Glu	Val	Phe	Arg	Leu	Pro	Gln	Glu	Glu	Glu	Glu
				950					955					960
Gly	Pro	Gly	Ala	Gly	Asp	Glu	Ser	Ser	Cys	Gly	Thr	Gly	Gly	Gly
				965					970					975
Thr	His	Arg	Arg	Ser	Lys	Lys	Ala	Lys	Ala	Pro	Glu	Arg	Pro	Gly
				980					985					990
Thr	Arg	Val	Ser	Glu	Arg	Leu	Arg	Gly	Ala	Arg	Ala	Glu	Thr	Gln
				995					1000					1005
Gly	Ala	Asn	His	Thr	Pro	Val	Ile	Ser	Ala	His	Gln	Thr	Arg	Ser
				1010					1015					1020
Thr	Thr	Thr	Pro	Pro	Arg	Cys	Ser	Pro	Ala	Arg	Glu	Arg	Val	Pro
				1025					1030					1035
Arg	Pro	Ala	Pro	Arg	Pro	Arg	Pro	Thr	Pro	Ala	Ser	Ala	Pro	Ala
				1040					1045					1050
Ala	Ile	Pro	Ala	Leu	Val	Pro	Val	Pro	Val	Ser	Ala	Pro	Val	Pro
				1055					1060					1065
Ile	Ser	Ala	Pro	Asn	Pro	Ile	Thr	Ile	Leu	Pro	Val	His	Ile	Leu
				1070					1075					1080
Pro	Ser	Pro	Pro	Pro	Pro	Ser	Gln	Ile	Pro	Pro	Cys	Ser	Ser	Pro
				1085					1090					1095
Ala	Cys	Thr	Pro	Pro	Pro	Ala	Cys	Thr	Pro	Pro	Pro	Ala	His	Thr
				1100					1105					1110
Pro	Pro	Pro	Ala	Gln	Thr	Cys	Leu	Val	Thr	Pro	Ser	Ser	Pro	Leu
				1115					1120					1125
Leu	Leu	Gly	Pro	Pro	Ser	Val	Pro	Ile	Ser	Ala	Ser	Val	Thr	Asn
				1130					1135					1140
Leu	Pro	Leu	Gly	Leu	Arg	Pro	Glu	Ala	Glu	Leu	Cys	Ala	Gln	Ala
				1145					1150					1155
Leu	Ala	Ser	Pro	Glu	Ser	Leu	Glu	Leu	Ala	Ser	Val	Ala	Ser	Ser
				1160					1165					1170
Glu	Thr	Ser	Ser	Leu	Ser	Leu	Val	Pro	Pro	Lys	Asp	Leu	Leu	Pro
				1175					1180					1185
Val	Ala	Val	Glu	Ile	Leu	Pro	Val	Ser	Glu	Lys	Asn	Leu	Ser	Leu
				1190					1195					1200
Thr	Pro	Ser	Ala	Pro	Ser	Leu	Thr	Leu	Glu	Ala	Gly	Ser	Ile	Pro
				1205					1210					1215
Asn	Gly	Gln	Glu	Gln	Glu	Ala	Pro	Asp	Ser	Ala	Glu	Gly	Thr	Thr
				1220					1225					1230
Leu	Thr	Val	Leu	Pro	Glu	Gly	Glu	Glu	Leu	Pro	Leu	Cys	Val	Ser
				1235					1240					1245
Glu	Ser	Asn	Gly	Leu	Glu	Leu	Pro	Pro	Ser	Ala	Ala	Ser	Asp	Glu
				1250					1255					1260
Pro	Leu	Gln	Glu	Pro	Leu	Glu	Ala	Asp	Arg	Thr	Ser	Glu	Glu	Leu
				1265					1270					1275
Thr	Glu	Ala	Lys	Thr	Pro	Thr	Ser	Ser	Pro	Glu	Lys	Pro	Gln	Glu

1280	1285	1290
Leu Val Thr Ala Glu Val Ala Ala Pro Ser Thr Ser Ser Ser Ala		
1295	1300	1305
Thr Ser Ser Pro Glu Gly Pro Ser Pro Ala Arg Pro Pro Arg Arg		
1310	1315	1320
Arg Thr Ser Ala Asp Val Glu Ile Arg Gly Gln Gly Thr Gly Arg		
1325	1330	1335
Pro Gly Gln Pro Pro Gly Pro Lys Val Leu Arg Lys Leu Pro Gly		
1340	1345	1350
Arg Leu Val Thr Val Val Glu Glu Lys Glu Leu Val Arg Arg Arg		
1355	1360	1365
Arg Gln Gln Arg Gly Ala Ala Ser Thr Leu Val Pro Gly Val Ser		
1370	1375	1380
Glu Thr Ser Ala Ser Pro Gly Ser Pro Ser Val Arg Ser Met Ser		
1385	1390	1395
Gly Pro Glu Ser Ser Pro Pro Ile Gly Gly Pro Cys Glu Ala Ala		
1400	1405	1410
Pro Ser Ser Ser Leu Pro Thr Pro Pro Gln Gln Pro Phe Ile Ala		
1415	1420	1425
Arg Arg His Ile Glu Leu Gly Val Thr Gly Gly Gly Ser Pro Glu		
1430	1435	1440
Asn Gly Asp Gly Ala Leu Leu Ala Ile Thr Pro Pro Ala Val Lys		
1445	1450	1455
Arg Arg Arg Gly Arg Pro Pro Lys Lys Asn Arg Ser Pro Ala Asp		
1460	1465	1470
Ala Gly Arg Gly Val Asp Glu Ala Pro Ser Ser Thr Leu Lys Gly		
1475	1480	1485
Lys Thr Asn Gly Ala Asp Pro Val Pro Gly Pro Glu Thr Leu Ile		
1490	1495	1500
Val Ala Asp Pro Val Leu Glu Pro Gln Leu Ile Pro Gly Pro Gln		
1505	1510	1515
Pro Leu Gly Pro Gln Pro Val His Arg Pro Asn Pro Leu Leu Ser		
1520	1525	1530
Pro Val Glu Lys Arg Arg Arg Gly Arg Pro Pro Lys Ala Arg Asp		
1535	1540	1545
Leu Pro Ile Pro Gly Thr Ile Ser Ser Ala Gly Asp Gly Asn Ser		
1550	1555	1560
Glu Ser Arg Thr Gln Pro Pro Pro His Pro Ser Pro Leu Thr Pro		
1565	1570	1575
Leu Pro Pro Leu Leu Val Cys Pro Thr Ala Thr Val Ala Asn Thr		
1580	1585	1590
Val Thr Thr Val Thr Ile Ser Thr Ser Pro Pro Lys Arg Lys Arg		
1595	1600	1605
Gly Arg Pro Pro Lys Asn Pro Pro Ser Pro Arg Pro Ser Gln Leu		
1610	1615	1620
Pro Val Leu Asp Arg Asp Ser Thr Ser Val Leu Glu Ser Cys Gly		
1625	1630	1635
Leu Gly Arg Arg Arg Gln Pro Gln Gly Gln Gly Glu Ser Glu Gly		
1640	1645	1650
Ser Ser Ser Asp Glu Asp Gly Ser Arg Pro Leu Thr Arg Leu Ala		
1655	1660	1665
Arg Leu Arg Leu Glu Ala Glu Gly Met Arg Gly Arg Lys Ser Gly		
1670	1675	1680
Gly Ser Met Val Val Ala Val Ile Gln Asp Asp Leu Asp Leu Ala		
1685	1690	1695
Asp Ser Gly Pro Gly Gly Leu Glu Leu Thr Pro Pro Val Val Ser		
1700	1705	1710
Leu Thr Pro Lys Leu Arg Ser Thr Arg Leu Arg Pro Gly Ser Leu		
1715	1720	1725
Val Pro Pro Leu Glu Thr Glu Lys Leu Pro Arg Lys Arg Ala Gly		
1730	1735	1740
Ala Pro Val Gly Gly Ser Pro Gly Leu Ala Lys Arg Gly Arg Leu		
1745	1750	1755

Gln Pro Pro Ser Pro Leu Gly Pro Glu Gly Ser Val Glu Glu Ser
 1760 1765 1770
 Glu Ala Glu Ala Ser Gly Glu Glu Glu Glu Gly Asp Gly Thr Pro
 1775 1780 1785
 Arg Arg Arg Pro Gly Pro Arg Arg Leu Val Gly Thr Thr Asn Gln
 1790 1795 1800
 Gly Asp Gln Arg Ile Leu Arg Ser Ser Ala Pro Pro Ser Leu Ala
 1805 1810 1815
 Gly Pro Ala Val Ser His Arg Gly Arg Lys Ala Lys Thr
 1820 1825

<210> 16
 <211> 482
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 975377CD1

<400> 16
 Met Ala Glu Ala Ala Thr Pro Gly Thr Thr Ala Thr Thr Ser Gly
 1 5 10 15
 Ala Gly Ala Ala Ala Ala Thr Ala Ala Ala Ala Ser Pro Thr Pro
 20 25 30
 Ile Pro Thr Val Thr Ala Pro Ser Leu Gly Ala Gly Gly Gly Gly
 35 40 45
 Gly Gly Ser Asp Gly Ser Gly Gly Gly Thr Lys Gln Val Thr
 50 55 60
 Cys Arg Tyr Phe Met His Gly Val Cys Lys Glu Gly Asp Asn Cys
 65 70 75
 Arg Tyr Ser His Asp Leu Ser Asp Ser Pro Tyr Ser Val Val Cys
 80 85 90
 Lys Tyr Phe Gln Arg Gly Tyr Cys Ile Tyr Gly Asp Arg Cys Arg
 95 100 105
 Tyr Glu His Ser Lys Pro Leu Lys Gln Glu Glu Ala Thr Ala Thr
 110 115 120
 Glu Leu Thr Thr Lys Ser Ser Leu Ala Ala Ser Ser Ser Leu Ser
 125 130 135
 Ser Ile Val Gly Pro Leu Val Glu Met Asn Thr Gly Glu Ala Glu
 140 145 150
 Ser Arg Asn Ser Asn Phe Ala Thr Val Gly Ala Gly Ser Glu Asp
 155 160 165
 Trp Val Asn Ala Ile Glu Phe Val Pro Gly Gln Pro Tyr Cys Gly
 170 175 180
 Arg Thr Ala Pro Ser Cys Thr Glu Ala Pro Leu Gln Gly Ser Val
 185 190 195
 Thr Lys Glu Glu Ser Glu Lys Glu Gln Thr Ala Val Glu Thr Lys
 200 205 210
 Lys Gln Leu Cys Pro Tyr Ala Ala Val Gly Glu Cys Arg Tyr Gly
 215 220 225
 Glu Asn Cys Val Tyr Leu His Gly Asp Ser Cys Asp Met Cys Gly
 230 235 240
 Leu Gln Val Leu His Pro Met Asp Ala Ala Gln Arg Ser Gln His
 245 250 255
 Ile Lys Ser Cys Ile Glu Ala His Glu Lys Asp Met Glu Leu Ser
 260 265 270
 Phe Ala Val Gln Arg Ser Lys Asp Met Val Cys Gly Ile Cys Met
 275 280 285
 Glu Val Val Tyr Glu Lys Ala Asn Pro Ser Glu Arg Arg Phe Gly
 290 295 300
 Ile Leu Ser Asn Cys Asn His Thr Tyr Cys Leu Lys Cys Ile Arg
 305 310 315

Lys	Trp	Arg	Ser	Ala	Lys	Gln	Phe	Glu	Ser	Lys	Ile	Ile	Lys	Ser	
				320					325					330	
Cys	Pro	Glu	Cys	Arg	Ile	Thr	Ser	Asn	Phe	Val	Ile	Pro	Ser	Glu	
				335					340					345	
Tyr	Trp	Val	Glu	Glu	Lys	Glu	Glu	Lys	Gln	Lys	Leu	Ile	Leu	Lys	
				350					355					360	
Tyr	Lys	Glu	Ala	Met	Ser	Asn	Lys	Ala	Cys	Arg	Tyr	Phe	Asp	Glu	
				365					370					375	
Gly	Arg	Gly	Ser	Cys	Pro	Phe	Gly	Gly	Asn	Cys	Phe	Tyr	Lys	His	
				380					385					390	
Ala	Tyr	Pro	Asp	Gly	Arg	Arg	Glu	Glu	Pro	Gln	Arg	Gln	Lys	Val	
				395					400					405	
Gly	Thr	Ser	Ser	Arg	Tyr	Arg	Ala	Gln	Arg	Arg	Asn	His	Phe	Trp	
				410					415					420	
Glu	Leu	Ile	Glu	Glu	Arg	Glu	Asn	Ser	Asn	Pro	Phe	Asp	Asn	Asp	
				425					430					435	
Glu	Glu	Glu	Val	Val	Thr	Phe	Glu	Leu	Gly	Glu	Met	Leu	Leu	Met	
				440					445					450	
Leu	Leu	Ala	Ala	Gly	Gly	Asp	Asp	Glu	Leu	Thr	Asp	Ser	Glu	Asp	
				455					460					465	
Glu	Trp	Asp	Leu	Phe	His	Asp	Glu	Leu	Glu	Asp	Phe	Tyr	Asp	Leu	
				470					475					480	
Asp	Leu														

<210> 17

<211> 264

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1208721CD1

<400> 17

Met	Leu	Gly	Ile	Leu	Ile	Tyr	Ile	Gln	Asn	Ser	Asp	Tyr	Glu	Glu	
1				5					10					15	
Ile	Thr	Ile	Asp	Pro	Thr	Cys	Ser	Trp	Lys	Pro	Val	Pro	Val	Lys	
				20					25					30	
Pro	Asp	Met	His	Ile	Lys	Glu	Glu	Pro	Asp	Gly	Pro	Ala	Leu	Lys	
				35					40					45	
Arg	Cys	Arg	Thr	Val	Ser	Pro	Ala	His	Val	Leu	Met	Pro	Ser	Val	
				50					55					60	
Met	Glu	Met	Ile	Ala	Ala	Leu	Gly	Pro	Gly	Ala	Ala	Pro	Phe	Ala	
				65					70					75	
Pro	Leu	Gln	Pro	Pro	Ser	Val	Pro	Ala	Pro	Ser	Asp	Tyr	Pro	Gly	
				80					85					90	
Gln	Gly	Ser	Ser	Phe	Leu	Gly	Pro	Gly	Thr	Phe	Pro	Glu	Ser	Phe	
				95					100					105	
Pro	Pro	Thr	Thr	Pro	Ser	Thr	Pro	Thr	Leu	Ala	Glu	Phe	Thr	Pro	
				110					115					120	
Gly	Pro	Pro	Pro	Ile	Ser	Tyr	Gln	Ser	Asp	Ile	Pro	Ser	Ser	Leu	
				125					130					135	
Leu	Thr	Ser	Glu	Lys	Ser	Thr	Ala	Cys	Leu	Pro	Ser	Gln	Met	Ala	
				140					145					150	
Pro	Ala	Gly	His	Leu	Asp	Pro	Thr	His	Asn	Pro	Gly	Thr	Pro	Gly	
				155					160					165	
Leu	His	Thr	Ser	Asn	Leu	Gly	Ala	Pro	Pro	Gly	Pro	Gln	Leu	His	
				170					175					180	
His	Ser	Asn	Pro	Pro	Pro	Ala	Ser	Arg	Gln	Ser	Leu	Gly	Gln	Ala	
				185					190					195	
Ser	Leu	Gly	Pro	Thr	Gly	Glu	Leu	Ala	Phe	Ser	Pro	Ala	Thr	Gly	
				200					205					210	

Val	Met	Gly	Pro	Pro	Ser	Met	Ser	Gly	Ala	Gly	Glu	Ala	Pro	Glu
				215					220					225
Pro	Ala	Leu	Asp	Leu	Leu	Pro	Glu	Leu	Thr	Asn	Pro	Asp	Glu	Leu
				230					235					240
Leu	Ser	Tyr	Leu	Gly	Pro	Pro	Asp	Leu	Pro	Thr	Asn	Asn	Asn	Asp
				245					250					255
Asp	Leu	Leu	Ser	Leu	Phe	Glu	Asn	Asn						
				260										

<210> 18

<211> 350

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1234329CD1

<400> 18

Met	Pro	Pro	Pro	Tyr	Ala	Ser	Leu	Thr	Arg	Pro	Leu	His	His	Gln
1				5					10					15
Ala	Ser	Ala	Cys	Pro	His	Ser	His	Gly	Asn	Pro	Pro	Pro	Gln	Thr
				20					25					30
Gln	Pro	Pro	Pro	Gln	Val	Asp	Tyr	Val	Ile	Pro	His	Pro	Val	His
				35					40					45
Ala	Phe	His	Ser	Gln	Ile	Ser	Ser	His	Ala	Thr	Ser	His	Pro	Val
				50					55					60
Ala	Pro	Pro	Pro	Pro	Thr	His	Leu	Ala	Ser	Thr	Ala	Ala	Pro	Ile
				65					70					75
Pro	Gln	His	Leu	Pro	Pro	Thr	His	Gln	Pro	Ile	Ser	His	His	Ile
				80					85					90
Pro	Ala	Thr	Ala	Pro	Pro	Ala	Gln	Arg	Leu	His	Pro	His	Glu	Val
				95					100					105
Met	Gln	Arg	Met	Glu	Val	Gln	Arg	Arg	Arg	Met	Met	Gln	His	Pro
				110					115					120
Thr	Gly	Leu	Phe	Val	Phe	Cys	Val	Ser	Arg	Arg	Ala	His	Glu	Arg
				125					130					135
Pro	Pro	Pro	His	Pro	His	Arg	Met	His	Pro	Asn	Tyr	Gly	His	Gly
				140					145					150
His	His	Ile	His	Val	Pro	Gln	Thr	Met	Ser	Ser	His	Pro	Arg	Gln
				155					160					165
Ala	Pro	Glu	Arg	Ser	Ala	Trp	Glu	Leu	Gly	Ile	Glu	Ala	Gly	Val
				170					175					180
Thr	Ala	Ala	Thr	Tyr	Thr	Pro	Gly	Ala	Leu	His	Pro	His	Leu	Ala
				185					190					195
His	Tyr	His	Ala	Pro	Pro	Arg	Leu	His	His	Leu	Gln	Leu	Gly	Ala
				200					205					210
Leu	Pro	Leu	Met	Val	Pro	Asp	Met	Ala	Gly	Tyr	Pro	His	Ile	Arg
				215					220					225
Tyr	Ile	Ser	Ser	Gly	Leu	Asp	Gly	Thr	Ser	Phe	Arg	Gly	Pro	Phe
				230					235					240
Arg	Gly	Asn	Phe	Glu	Glu	Leu	Ile	His	Leu	Glu	Glu	Arg	Leu	Gly
				245					250					255
Asn	Val	Asn	Arg	Gly	Ala	Ser	Gln	Gly	Thr	Ile	Glu	Arg	Cys	Thr
				260					265					270
Tyr	Pro	His	Lys	Tyr	Lys	Lys	Arg	Lys	Leu	His	Cys	Lys	Gln	Asp
				275					280					285
Gly	Glu	Glu	Gly	Thr	Glu	Glu	Asp	Thr	Glu	Glu	Lys	Cys	Thr	Ile
				290					295					300
Cys	Leu	Ser	Ile	Leu	Glu	Glu	Gly	Glu	Asp	Val	Arg	Arg	Leu	Pro
				305					310					315
Cys	Met	His	Leu	Phe	His	Gln	Val	Cys	Val	Asp	Gln	Trp	Leu	Ile
				320					325					330

Thr Asn Lys Lys Cys Pro Ile Cys Arg Val Asp Ile Glu Ala Gln
 335 340 345
 Leu Pro Ser Glu Ser
 350

<210> 19
 <211> 549
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1238747CD1

<400> 19
 Met Phe Thr Met Thr Arg Ala Met Glu Glu Ala Leu Phe Gln His
 1 5 10 15
 Phe Met His Gln Lys Leu Gly Ile Ala Tyr Ala Ile His Lys Pro
 20 25 30
 Phe Pro Phe Phe Glu Gly Leu Leu Asp Asn Ser Ile Ile Thr Lys
 35 40 45
 Arg Met Tyr Met Glu Ser Leu Glu Ala Cys Arg Asn Leu Ile Pro
 50 55 60
 Val Ser Arg Val Val His Asn Ile Leu Thr Gln Leu Glu Arg Thr
 65 70 75
 Phe Asn Leu Ser Leu Leu Val Thr Leu Phe Ser Gln Ile Asn Leu
 80 85 90
 Arg Glu Tyr Pro Asn Leu Val Thr Ile Tyr Arg Ser Phe Lys Arg
 95 100 105
 Val Gly Ala Ser Tyr Glu Arg Gln Ser Arg Asp Thr Pro Ile Leu
 110 115 120
 Leu Glu Ala Pro Thr Gly Leu Ala Glu Gly Ser Ser Leu His Thr
 125 130 135
 Pro Leu Ala Leu Pro Pro Pro Gln Pro Pro Gln Pro Ser Cys Ser
 140 145 150
 Pro Cys Ala Pro Arg Val Ser Glu Pro Gly Thr Ser Ser Gln Gln
 155 160 165
 Ser Asp Glu Ile Leu Ser Glu Ser Pro Ser Pro Ser Asp Pro Val
 170 175 180
 Leu Pro Leu Pro Ala Leu Ile Gln Glu Gly Arg Ser Thr Ser Val
 185 190 195
 Thr Asn Asp Lys Leu Thr Ser Lys Met Asn Ala Glu Glu Asp Ser
 200 205 210
 Glu Glu Met Pro Ser Leu Leu Thr Ser Thr Val Gln Val Ala Ser
 215 220 225
 Asp Asn Leu Ile Pro Gln Ile Arg Asp Lys Glu Asp Pro Gln Glu
 230 235 240
 Met Pro His Ser Pro Leu Gly Ser Met Pro Glu Ile Arg Asp Asn
 245 250 255
 Ser Pro Glu Pro Asn Asp Pro Glu Glu Pro Gln Glu Val Ser Ser
 260 265 270
 Thr Pro Ser Asp Lys Lys Gly Lys Lys Arg Lys Arg Cys Ile Trp
 275 280 285
 Ser Thr Pro Lys Arg Arg His Lys Lys Lys Ser Leu Pro Arg Gly
 290 295 300
 Thr Ala Ser Ser Arg His Gly Ile Gln Lys Lys Leu Lys Arg Val
 305 310 315
 Asp Gln Val Pro Gln Lys Lys Asp Asp Ser Thr Cys Asn Ser Thr
 320 325 330
 Val Glu Thr Arg Ala Gln Lys Ala Arg Thr Glu Cys Ala Arg Lys
 335 340 345
 Ser Arg Ser Glu Glu Ile Ile Asp Gly Thr Ser Glu Met Asn Glu
 350 355 360

Gly	Lys	Arg	Ser	Gln	Lys	Thr	Pro	Ser	Thr	Pro	Arg	Arg	Val	Thr	
				365					370					375	
Gln	Gly	Ala	Ala	Ser	Pro	Gly	His	Gly	Ile	Gln	Glu	Lys	Leu	Gln	
				380					385					390	
Val	Val	Asp	Lys	Val	Thr	Gln	Arg	Lys	Asp	Asp	Ser	Thr	Trp	Asn	
				395					400					405	
Ser	Glu	Val	Met	Met	Arg	Val	Gln	Lys	Ala	Arg	Thr	Lys	Cys	Ala	
				410					415					420	
Arg	Lys	Ser	Arg	Ser	Lys	Glu	Lys	Lys	Lys	Glu	Lys	Asp	Ile	Cys	
				425					430					435	
Ser	Ser	Ser	Lys	Arg	Arg	Phe	Gln	Lys	Asn	Ile	His	Arg	Arg	Gly	
				440					445					450	
Lys	Pro	Lys	Ser	Asp	Thr	Val	Asp	Phe	His	Cys	Ser	Lys	Leu	Pro	
				455					460					465	
Val	Thr	Cys	Gly	Glu	Ala	Lys	Gly	Ile	Leu	Tyr	Lys	Lys	Lys	Met	
				470					475					480	
Lys	His	Gly	Ser	Ser	Val	Lys	Cys	Ile	Arg	Asn	Glu	Asp	Gly	Thr	
				485					490					495	
Trp	Leu	Thr	Pro	Asn	Glu	Phe	Glu	Val	Glu	Gly	Lys	Gly	Arg	Asn	
				500					505					510	
Ala	Lys	Asn	Trp	Lys	Arg	Asn	Ile	Arg	Cys	Glu	Gly	Met	Thr	Leu	
				515					520					525	
Gly	Glu	Leu	Leu	Lys	Ser	Gly	Leu	Leu	Leu	Cys	Pro	Pro	Arg	Ile	
				530					535					540	
Asn	Leu	Lys	Arg	Glu	Leu	Asn	Ser	Lys							
				545											

<210> 20

<211> 337

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1265980CD1

<400> 20

Met	Leu	Thr	Leu	Pro	Phe	Asp	Glu	Ser	Val	Val	Met	Pro	Glu	Ser	
1				5					10					15	
Gln	Met	Cys	Arg	Lys	Phe	Ser	Arg	Glu	Cys	Glu	Asp	Gln	Lys	Gln	
				20					25					30	
Ile	Lys	Lys	Pro	Glu	Ser	Phe	Ser	Lys	Gln	Ile	Val	Leu	Arg	Gly	
				35					40					45	
Lys	Ser	Ile	Lys	Arg	Ala	Pro	Gly	Glu	Glu	Thr	Glu	Lys	Glu	Glu	
				50					55					60	
Glu	Glu	Glu	Asp	Arg	Glu	Glu	Glu	Asp	Glu	Asn	Gly	Leu	Pro	Arg	
				65					70					75	
Arg	Arg	Gly	Leu	Arg	Lys	Lys	Lys	Thr	Thr	Lys	Leu	Arg	Leu	Glu	
				80					85					90	
Arg	Val	Lys	Phe	Arg	Arg	Gln	Glu	Ala	Asn	Ala	Arg	Glu	Arg	Asn	
				95					100					105	
Arg	Met	His	Gly	Leu	Asn	Asp	Ala	Leu	Asp	Asn	Leu	Arg	Lys	Val	
				110					115					120	
Val	Pro	Cys	Tyr	Ser	Arg	Thr	Gln	Lys	Leu	Ser	Lys	Ile	Glu	Thr	
				125					130					135	
Leu	Arg	Leu	Ala	Lys	Asn	Tyr	Ile	Trp	Ala	Leu	Ser	Glu	Ile	Leu	
				140					145					150	
Arg	Ile	Gly	Lys	Arg	Pro	Asp	Leu	Leu	Thr	Phe	Val	Gln	Asn	Leu	
				155					160					165	
Cys	Lys	Gly	Leu	Ser	Gln	Pro	Thr	Thr	Asn	Leu	Val	Ala	Gly	Cys	
				170					175					180	
Leu	Gln	Leu	Asn	Ala	Arg	Ser	Phe	Leu	Met	Gly	Gln	Gly	Gly	Glu	
				185					190					195	

Ala	Ala	His	His	Thr	Arg	Ser	Pro	Tyr	Ser	Thr	Phe	Tyr	Pro	Pro
				200					205					210
Tyr	His	Ser	Pro	Glu	Leu	Thr	Thr	Pro	Pro	Gly	His	Gly	Thr	Leu
				215					220					225
Asp	Asn	Ser	Lys	Ser	Met	Lys	Pro	Tyr	Asn	Tyr	Cys	Ser	Ala	Tyr
				230					235					240
Glu	Ser	Phe	Tyr	Glu	Ser	Thr	Ser	Pro	Glu	Cys	Ala	Ser	Pro	Gln
				245					250					255
Phe	Glu	Gly	Pro	Leu	Ser	Pro	Pro	Pro	Ile	Asn	Tyr	Asn	Gly	Ile
				260					265					270
Phe	Ser	Leu	Lys	Gln	Glu	Glu	Thr	Leu	Asp	Tyr	Gly	Lys	Asn	Tyr
				275					280					285
Asn	Tyr	Gly	Met	His	Tyr	Cys	Ala	Val	Pro	Pro	Arg	Gly	Pro	Leu
				290					295					300
Gly	Gln	Gly	Ala	Met	Phe	Arg	Leu	Pro	Thr	Asp	Ser	His	Phe	Pro
				305					310					315
Tyr	Asp	Leu	His	Leu	Arg	Ser	Gln	Ser	Leu	Thr	Met	Gln	Asp	Glu
				320					325					330
Leu	Asn	Ala	Val	Phe	His	Asn								
				335										

<210> 21

<211> 581

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1297333CD1

<400> 21

Met	Val	Lys	Arg	Glu	Leu	Thr	Gly	Ser	Leu	Phe	Ser	Gly	Gln	Arg
1				5					10					15
Ser	Val	His	Glu	Thr	Gln	Glu	Leu	Phe	Pro	Lys	Gln	Asp	Ser	Tyr
				20					25					30
Ala	Glu	Gly	Val	Thr	Asp	Arg	Thr	Ser	Asn	Thr	Lys	Leu	Asp	Cys
				35					40					45
Ser	Ser	Phe	Arg	Glu	Asn	Trp	Asp	Ser	Asp	Tyr	Val	Phe	Gly	Arg
				50					55					60
Lys	Leu	Ala	Val	Gly	Gln	Glu	Thr	Gln	Phe	Arg	Gln	Glu	Pro	Ile
				65					70					75
Thr	His	Asn	Lys	Thr	Leu	Ser	Lys	Glu	Arg	Glu	Arg	Thr	Tyr	Asn
				80					85					90
Lys	Ser	Gly	Arg	Trp	Phe	Tyr	Leu	Asp	Asp	Ser	Glu	Glu	Lys	Val
				95					100					105
His	Asn	Arg	Asp	Ser	Ile	Lys	Asn	Phe	Gln	Lys	Ser	Ser	Val	Val
				110					115					120
Ile	Lys	Gln	Thr	Gly	Ile	Tyr	Ala	Gly	Lys	Lys	Leu	Phe	Lys	Cys
				125					130					135
Asn	Glu	Cys	Lys	Lys	Thr	Phe	Thr	Gln	Ser	Ser	Ser	Leu	Thr	Val
				140					145					150
His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Asn	Glu
				155					160					165
Cys	Gly	Lys	Ala	Phe	Ser	Asp	Gly	Ser	Ser	Phe	Ala	Arg	His	Gln
				170					175					180
Arg	Cys	His	Thr	Gly	Lys	Lys	Pro	Tyr	Glu	Cys	Ile	Glu	Cys	Gly
				185					190					195
Lys	Ala	Phe	Ile	Gln	Asn	Thr	Ser	Leu	Ile	Arg	His	Trp	Arg	Tyr
				200					205					210
Tyr	His	Thr	Gly	Glu	Lys	Pro	Phe	Asp	Cys	Ile	Asp	Cys	Gly	Lys
				215					220					225
Ala	Phe	Ser	Asp	His	Ile	Gly	Leu	Asn	Gln	His	Arg	Arg	Ile	His
				230					235					240

Thr Gly Glu Lys Pro Tyr Lys Cys Asp Val Cys His Lys Ser Phe
 245 250 255
 Arg Tyr Gly Ser Ser Leu Thr Val His Gln Arg Ile His Thr Gly
 260 265 270
 Glu Lys Pro Tyr Glu Cys Asp Val Cys Arg Lys Ala Phe Ser His
 275 280 285
 His Ala Ser Leu Thr Gln His Gln Arg Val His Ser Gly Glu Lys
 290 295 300
 Pro Phe Lys Cys Lys Glu Cys Gly Lys Ala Phe Arg Gln Asn Ile
 305 310 315
 His Leu Ala Ser His Leu Arg Ile His Thr Gly Glu Lys Pro Phe
 320 325 330
 Glu Cys Ala Glu Cys Gly Lys Ser Phe Ser Ile Ser Ser Gln Leu
 335 340 345
 Ala Thr His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys
 350 355 360
 Lys Val Cys Ser Lys Ala Phe Thr Gln Lys Ala His Leu Ala Gln
 365 370 375
 His Gln Lys Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu
 380 385 390
 Cys Gly Lys Ala Phe Ser Gln Thr Thr His Leu Ile Gln His Gln
 395 400 405
 Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys Met Glu Cys Gly
 410 415 420
 Lys Ala Phe Gly Asp Asn Ser Ser Cys Thr Gln His Gln Arg Leu
 425 430 435
 His Thr Gly Gln Arg Pro Tyr Glu Cys Ile Glu Cys Gly Lys Ala
 440 445 450
 Phe Lys Thr Lys Ser Ser Leu Ile Cys His Arg Arg Ser His Thr
 455 460 465
 Gly Glu Lys Pro Tyr Glu Cys Ser Val Cys Gly Lys Ala Phe Ser
 470 475 480
 His Arg Gln Ser Leu Ser Val His Gln Arg Ile His Ser Gly Lys
 485 490 495
 Lys Pro Tyr Glu Cys Lys Glu Cys Arg Lys Thr Phe Ile Gln Ile
 500 505 510
 Gly His Leu Asn Gln His Lys Arg Val His Thr Gly Glu Arg Ser
 515 520 525
 Tyr Asn Tyr Lys Lys Ser Arg Lys Val Phe Arg Gln Thr Ala His
 530 535 540
 Leu Ala His His Gln Arg Ile His Thr Gly Glu Ser Ser Thr Cys
 545 550 555
 Pro Ser Leu Pro Ser Thr Ser Asn Pro Val Asp Leu Phe Pro Lys
 560 565 570
 Phe Leu Trp Asn Pro Ser Ser Leu Pro Ser Pro
 575 580

<210> 22

<211> 591

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1312824CD1

<400> 22

Met Ala Ala Val Val Gln Gln Asn Asp Leu Val Phe Glu Phe Ala
 1 5 10 15
 Ser Asn Val Met Glu Asp Glu Arg Gln Leu Gly Asp Pro Ala Ile
 20 25 30
 Phe Pro Ala Val Ile Val Glu His Val Pro Gly Ala Asp Ile Leu
 35 40 45

Asn	Ser	Tyr	Ala	Gly	Leu	Ala	Cys	Val	Glu	Glu	Pro	Ser	Asp	Met
				50					55					60
Ile	Thr	Glu	Ser	Ser	Leu	Asp	Val	Ala	Glu	Glu	Ile	Ile	Asp	
				65					70					75
Asp	Asp	Asp	Asp	Asp	Ile	Thr	Leu	Thr	Val	Glu	Ala	Ser	Cys	His
				80					85					90
Asp	Gly	Asp	Glu	Thr	Ile	Glu	Thr	Ile	Glu	Ala	Ala	Glu	Ala	Leu
				95					100					105
Leu	Asn	Met	Asp	Ser	Pro	Gly	Pro	Met	Leu	Asp	Glu	Lys	Arg	Ile
				110					115					120
Asn	Asn	Asn	Ile	Phe	Ser	Ser	Pro	Glu	Asp	Asp	Met	Val	Val	Ala
				125					130					135
Pro	Val	Thr	His	Val	Ser	Val	Thr	Leu	Asp	Gly	Ile	Pro	Glu	Val
				140					145					150
Met	Glu	Thr	Gln	Gln	Val	Gln	Glu	Lys	Tyr	Ala	Asp	Ser	Pro	Gly
				155					160					165
Ala	Ser	Ser	Pro	Glu	Gln	Pro	Lys	Arg	Lys	Lys	Gly	Asn	Thr	Ile
				170					175					180
Tyr	Leu	Trp	Glu	Phe	Leu	Leu	Ala	Leu	Leu	Gln	Asp	Lys	Ala	Thr
				185					190					195
Cys	Pro	Lys	Tyr	Ile	Lys	Trp	Thr	Gln	Arg	Glu	Lys	Gly	Ile	Phe
				200					205					210
Lys	Leu	Val	Asp	Ser	Lys	Ala	Val	Ser	Arg	Leu	Trp	Gly	Lys	His
				215					220					225
Lys	Asn	Lys	Pro	Asp	Met	Asn	Tyr	Glu	Thr	Met	Gly	Arg	Ala	Leu
				230					235					240
Arg	Tyr	Tyr	Tyr	Gln	Arg	Gly	Ile	Leu	Ala	Lys	Val	Glu	Gly	Gln
				245					250					255
Arg	Leu	Val	Tyr	Gln	Phe	Lys	Glu	Met	Pro	Lys	Asp	Leu	Ile	Tyr
				260					265					270
Ile	Asn	Asp	Glu	Asp	Pro	Ser	Ser	Ser	Ile	Glu	Ser	Ser	Asp	Pro
				275					280					285
Ser	Leu	Ser	Ser	Ser	Ala	Thr	Ser	Asn	Arg	Asn	Gln	Thr	Ser	Arg
				290					295					300
Ser	Arg	Val	Ser	Ser	Ser	Pro	Gly	Val	Lys	Gly	Gly	Ala	Thr	Ser
				305					310					315
Val	Leu	Lys	Pro	Gly	Asn	Ser	Lys	Ala	Ala	Lys	Pro	Lys	Asp	Pro
				320					325					330
Val	Glu	Val	Ala	Gln	Pro	Ser	Glu	Val	Leu	Arg	Thr	Val	Gln	Pro
				335					340					345
Thr	Gln	Ser	Pro	Tyr	Pro	Thr	Gln	Leu	Phe	Arg	Thr	Val	His	Val
				350					355					360
Val	Gln	Pro	Val	Gln	Ala	Val	Pro	Glu	Gly	Glu	Ala	Ala	Arg	Thr
				365					370					375
Ser	Thr	Met	Gln	Asp	Glu	Thr	Leu	Asn	Ser	Ser	Val	Gln	Ser	Ile
				380					385					390
Arg	Thr	Ile	Gln	Ala	Pro	Thr	Gln	Val	Pro	Val	Val	Val	Ser	Pro
				395					400					405
Arg	Asn	Gln	Gln	Leu	His	Thr	Val	Thr	Leu	Gln	Thr	Val	Pro	Leu
				410					415					420
Thr	Thr	Val	Ile	Ala	Ser	Thr	Asp	Pro	Ser	Ala	Gly	Thr	Gly	Ser
				425					430					435
Gln	Lys	Phe	Ile	Leu	Gln	Ala	Ile	Pro	Ser	Ser	Gln	Pro	Met	Thr
				440					445					450
Val	Leu	Lys	Glu	Asn	Val	Met	Leu	Gln	Ser	Gln	Lys	Ala	Gly	Ser
				455					460					465
Pro	Pro	Ser	Ile	Val	Leu	Gly	Pro	Ala	Gln	Val	Gln	Gln	Val	Leu
				470					475					480
Thr	Ser	Asn	Val	Gln	Thr	Ile	Cys	Asn	Gly	Thr	Val	Ser	Val	Ala
				485					490					495
Ser	Ser	Pro	Ser	Phe	Ser	Ala	Thr	Ala	Pro	Val	Val	Thr	Phe	Ser
				500					505					510
Pro	Arg	Ser	Ser	Gln	Leu	Val	Ala	His	Pro	Pro	Gly	Thr	Val	Ile

Thr Ser Val Ile	515	Thr Gln Glu Thr	520	Thr Leu Thr Gln	525
	Lys		Lys		Glu
Val Glu Lys Lys	530	Ser Glu Asp His	535	Leu Lys Glu Asn Thr	540
	Glu		Leu		Glu
Lys Thr Glu Gln	545	Pro Gln Pro Tyr	550	Val Met Val Val Ser	555
	Gln		Val		Ser
Ser Asn Gly Phe	560	Thr Ser Gln Val Ala	565	Lys Gln Asn Glu	570
	Thr		Met		Leu
Leu Glu Pro Asn Ser	575		580		585
	Phe				
	590				

<210> 23
 <211> 767
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1359294CD1

<400> 23

Met Ser Phe Asp Pro	Asn Leu Leu His	Asn Asn Gly His	Asn Gly
1	5	10	15
Tyr Pro Asn Gly Thr	Ser Ala Ala Leu	Arg Glu Thr Gly	Val Ile
	20	25	30
Glu Lys Leu Leu Thr	Ser Tyr Gly Phe	Ile Gln Cys Ser	Glu Arg
	35	40	45
Gln Ala Arg Leu Phe	His Cys Ser Gln	Tyr Asn Gly Asn	Leu
	50	55	60
Gln Asp Leu Lys Val	Gly Asp Asp Val	Glu Phe Glu Val	Ser Ser
	65	70	75
Asp Arg Arg Thr Gly	Lys Pro Ile Ala	Val Lys Leu Val	Lys Ile
	80	85	90
Lys Gln Glu Ile Leu	Pro Glu Glu Arg	Met Asn Gly Gln	Glu Val
	95	100	105
Phe Tyr Leu Thr Tyr	Thr Pro Glu Asp	Val Glu Gly Asn	Val Gln
	110	115	120
Leu Glu Thr Gly Asp	Lys Ile Asn Phe	Val Ile Asp Asn	Asn Lys
	125	130	135
His Thr Gly Ala Val	Ser Ala Arg Asn	Ile Met Leu Leu	Lys Lys
	140	145	150
Lys Gln Ala Arg Cys	Gln Gly Val Val	Cys Ala Met Lys	Glu Ala
	155	160	165
Phe Gly Phe Ile Glu	Arg Gly Asp Val	Val Lys Glu Ile	Phe Phe
	170	175	180
His Tyr Ser Glu Phe	Lys Gly Asp Leu	Glu Thr Leu Gln	Pro Gly
	185	190	195
Asp Asp Val Glu Phe	Thr Ile Lys Asp	Arg Asn Gly Lys	Glu Val
	200	205	210
Ala Thr Asp Val Arg	Leu Leu Pro Gln	Gly Thr Val Ile	Phe Glu
	215	220	225
Asp Ile Ser Ile Glu	His Phe Glu Gly	Thr Val Thr Lys	Val Ile
	230	235	240
Pro Lys Val Pro Ser	Lys Asn Gln Asn	Asp Pro Leu Pro	Gly Arg
	245	250	255
Ile Lys Val Asp Phe	Val Ile Pro Lys	Glu Leu Pro Phe	Gly Asp
	260	265	270
Lys Asp Thr Lys Ser	Lys Val Thr Leu	Leu Glu Gly Asp	His Val
	275	280	285
Arg Phe Asn Ile Ser	Thr Asp Arg Arg	Asp Lys Leu Glu	Arg Ala
	290	295	300
Thr Asn Ile Glu Val	Leu Ser Asn Thr	Phe Gln Phe Thr	Asn Glu

	305		310		315
Ala Arg Glu Met Gly	Val Ile Ala Ala Met Arg Asp Gly Phe Gly				
	320		325		330
Phe Ile Lys Cys Val	Asp Arg Asp Val Arg Met Phe Phe His Phe				
	335		340		345
Ser Glu Ile Leu Asp	Gly Asn Gln Leu His Ile Ala Asp Glu Val				
	350		355		360
Glu Phe Thr Val Val	Pro Asp Met Leu Ser Ala Gln Arg Asn His				
	365		370		375
Ala Ile Arg Ile Lys	Lys Leu Pro Lys Gly Thr Val Ser Phe His				
	380		385		390
Ser His Ser Asp His	Arg Phe Leu Gly Thr Val Glu Lys Glu Ala				
	395		400		405
Thr Phe Ser Asn Pro	Lys Thr Thr Ser Pro Asn Lys Gly Lys Glu				
	410		415		420
Lys Glu Ala Glu Asp	Gly Ile Ile Ala Tyr Asp Asp Cys Gly Val				
	425		430		435
Lys Leu Thr Ile Ala	Phe Gln Ala Lys Asp Val Glu Gly Ser Thr				
	440		445		450
Ser Pro Gln Ile Gly	Asp Lys Val Glu Phe Ser Ile Ser Asp Lys				
	455		460		465
Gln Arg Pro Gly Gln	Gln Val Ala Thr Cys Val Arg Leu Leu Gly				
	470		475		480
Arg Asn Ser Asn Ser	Lys Arg Leu Leu Gly Tyr Val Ala Thr Leu				
	485		490		495
Lys Asp Asn Phe Gly	Phe Ile Glu Thr Ala Asn His Asp Lys Glu				
	500		505		510
Ile Phe Phe His Tyr	Ser Glu Phe Ser Gly Asp Val Asp Ser Leu				
	515		520		525
Glu Leu Gly Asp Met	Val Glu Tyr Ser Leu Ser Lys Gly Lys Gly				
	530		535		540
Asn Lys Val Ser Ala	Glu Lys Val Asn Lys Thr His Ser Val Asn				
	545		550		555
Gly Ile Thr Glu Glu	Ala Asp Pro Thr Ile Tyr Ser Gly Lys Val				
	560		565		570
Ile Arg Pro Leu Arg	Ser Val Asp Pro Thr Gln Thr Glu Tyr Gln				
	575		580		585
Gly Met Ile Glu Ile	Val Glu Glu Gly Asp Met Lys Gly Glu Val				
	590		595		600
Tyr Pro Phe Gly Ile	Val Gly Met Ala Asn Lys Gly Asp Cys Leu				
	605		610		615
Gln Lys Gly Glu Ser	Val Lys Phe Gln Leu Cys Val Leu Gly Gln				
	620		625		630
Asn Ala Gln Thr Met	Ala Tyr Asn Ile Thr Pro Leu Arg Arg Ala				
	635		640		645
Thr Val Glu Cys Val	Lys Asp Gln Phe Gly Phe Ile Asn Tyr Glu				
	650		655		660
Val Gly Asp Ser Lys	Lys Leu Phe Phe His Val Lys Glu Val Gln				
	665		670		675
Asp Gly Ile Glu Leu	Gln Ala Gly Asp Glu Val Glu Phe Ser Val				
	680		685		690
Ile Leu Asn Gln Arg	Thr Gly Lys Cys Ser Ala Cys Asn Val Trp				
	695		700		705
Arg Val Cys Glu Gly	Pro Lys Ala Val Ala Ala Pro Arg Pro Asp				
	710		715		720
Arg Leu Val Asn Arg	Leu Lys Asn Ile Thr Leu Asp Asp Ala Ser				
	725		730		735
Ala Pro Arg Leu Met	Val Leu Arg Gln Pro Arg Gly Pro Asp Asn				
	740		745		750
Ser Met Gly Phe Gly	Ala Glu Arg Lys Ile Arg Gln Ala Gly Val				
	755		760		765
Ile Asp					

<210> 24

<211> 206

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1377380CD1

<400> 24

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Met Ser Pro Arg Lys Ala Leu Ile Pro Val Ser Gln Lys Ser Ser
 1          5          10          15
Gln Ala Glu Ala Cys Ser Glu Ser Arg Asn Arg Val Lys Arg Arg
          20          25          30
Leu Asp Ser Ser Cys Leu Glu Ser Val Lys Gln Lys Cys Val Lys
          35          40          45
Ser Cys Asn Cys Val Thr Glu Leu Asp Gly Gln Val Glu Asn Leu
          50          55          60
His Leu Asp Leu Cys Cys Leu Ala Gly Asn Gln Glu Asp Leu Ser
          65          70          75
Lys Asp Ser Leu Gly Pro Thr Lys Ser Ser Lys Ile Glu Gly Ala
          80          85          90
Gly Thr Ser Ile Ser Glu Pro Pro Ser Pro Ile Ser Pro Tyr Ala
          95          100          105
Ser Glu Ser Cys Gly Thr Leu Pro Leu Pro Leu Arg Pro Cys Gly
          110          115          120
Glu Gly Ser Glu Met Val Gly Lys Glu Asn Ser Ser Pro Glu Asn
          125          130          135
Lys Asn Trp Leu Leu Ala Met Ala Ala Lys Arg Lys Ala Glu Asn
          140          145          150
Pro Ser Pro Arg Ser Pro Ser Ser Gln Thr Pro Asn Ser Arg Arg
          155          160          165
Gln Ser Gly Lys Thr Leu Pro Ser Pro Val Thr Ile Thr Pro Ser
          170          175          180
Ser Met Arg Lys Ile Cys Thr Tyr Phe His Arg Lys Ser Gln Glu
          185          190          195
Asp Phe Cys Gly Pro Glu His Ser Thr Glu Leu
          200          205

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<210> 25

<211> 352

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1383473CD1

<400> 25

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Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu
 1          5          10          15
Gly Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg
          20          25          30
Gln Lys Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val
          35          40          45
His Leu Gly Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly
          50          55          60
Lys Cys Val Pro Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val
          65          70          75
Lys Glu Thr Leu Asn Ser Gln Phe Val Glu Asn Cys Lys Gly Val
          80          85          90
Ile Gln Arg Leu Thr Leu Gln Glu His Lys Met Val Trp Asn Arg
          95          100          105

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Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile Ile His Gln Arg
110 115 120
Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu Asp Gly Val
125 130 135
Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val Asp Leu
140 145 150
Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln Ser
155 160 165
Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
170 175 180
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu
185 190 195
Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu
200 205 210
Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp
215 220 225
Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
230 235 240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu
245 250 255
Phe Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu
260 265 270
Arg Leu Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln
275 280 285
Leu Leu Ser Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser
290 295 300
Ala Cys Val Val Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu
305 310 315
Glu Cys Gly His Val Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu
320 325 330
Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg Gln Ala Ile Thr Arg
335 340 345
Val Ile Pro Leu Tyr Asn Ser
350

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<210> 26

<211> 532

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1388860CD1

<400> 26

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Met Met Phe Gln Asp Ser Val Ala Phe Glu Asp Val Ala Val Ser
1 5 10 15
Phe Thr Gln Glu Glu Trp Ala Leu Leu Asp Pro Ser Gln Lys Asn
20 25 30
Leu Tyr Arg Asp Val Met Gln Glu Thr Phe Lys Asn Leu Thr Ser
35 40 45
Val Gly Lys Thr Trp Lys Val Gln Asn Ile Glu Asp Glu Tyr Lys
50 55 60
Asn Pro Arg Arg Asn Leu Ser Leu Met Arg Glu Lys Leu Cys Glu
65 70 75
Ser Lys Glu Ser His His Cys Gly Glu Ser Phe Asn Gln Ile Ala
80 85 90
Asp Asp Met Leu Asn Arg Lys Thr Leu Pro Gly Ile Thr Pro Cys
95 100 105
Glu Ser Ser Val Cys Gly Glu Val Gly Thr Gly His Ser Ser Leu
110 115 120
Asn Thr His Ile Arg Ala Asp Thr Gly His Lys Ser Ser Glu Tyr
125 130 135

```

Gln	Glu	Tyr	Gly	Glu	Asn	Pro	Tyr	Arg	Asn	Lys	Glu	Cys	Lys	Lys
				140					145					150
Ala	Phe	Ser	Tyr	Leu	Asp	Ser	Leu	Gln	Ser	His	Asp	Lys	Ala	Cys
				155					160					165
Thr	Lys	Glu	Lys	Pro	Tyr	Asp	Gly	Lys	Glu	Cys	Thr	Glu	Thr	Phe
				170					175					180
Ile	Ser	His	Ser	Cys	Ile	Gln	Arg	His	Arg	Val	Met	His	Ser	Gly
				185					190					195
Asp	Gly	Pro	Tyr	Lys	Cys	Lys	Phe	Cys	Gly	Lys	Ala	Phe	Tyr	Phe
				200					205					210
Leu	Asn	Leu	Cys	Leu	Ile	His	Glu	Arg	Ile	His	Thr	Gly	Val	Lys
				215					220					225
Pro	Tyr	Lys	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Thr
				230					235					240
Thr	Leu	Pro	Val	His	Glu	Arg	Thr	His	Thr	Gly	Val	Asn	Ala	Asp
				245					250					255
Glu	Cys	Lys	Glu	Cys	Gly	Asn	Ala	Phe	Ser	Phe	Pro	Ser	Glu	Ile
				260					265					270
Arg	Arg	His	Lys	Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys
				275					280					285
Lys	Gln	Cys	Gly	Lys	Val	Phe	Ile	Ser	Phe	Ser	Ser	Ile	Gln	Tyr
				290					295					300
His	Lys	Met	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln
				305					310					315
Cys	Gly	Lys	Ala	Phe	Arg	Cys	Gly	Ser	His	Leu	Gln	Lys	His	Gly
				320					325					330
Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Arg	Gln	Cys	Gly
				335					340					345
Lys	Ala	Phe	Arg	Cys	Thr	Ser	Asp	Leu	Gln	Arg	His	Glu	Lys	Thr
				350					355					360
His	Thr	Glu	Asp	Lys	Pro	Tyr	Gly	Cys	Lys	Gln	Cys	Gly	Lys	Gly
				365					370					375
Phe	Arg	Cys	Ala	Ser	Gln	Leu	Gln	Ile	His	Glu	Arg	Thr	His	Ser
				380					385					390
Gly	Glu	Lys	Pro	His	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Val	Phe	Lys
				395					400					405
Tyr	Phe	Ser	Ser	Leu	Arg	Ile	His	Glu	Arg	Thr	His	Thr	Gly	Glu
				410					415					420
Lys	Pro	His	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Tyr	Phe
				425					430					435
Ser	Ser	Leu	His	Ile	His	Glu	Arg	Thr	His	Thr	Gly	Asp	Lys	Pro
				440					445					450
Tyr	Glu	Cys	Lys	Val	Cys	Gly	Lys	Ala	Phe	Thr	Cys	Ser	Ser	Ser
				455					460					465
Ile	Arg	Tyr	His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu
				470					475					480
Cys	Lys	His	Cys	Gly	Lys	Ala	Phe	Ile	Ser	Asn	Tyr	Ile	Arg	Tyr
				485					490					495
His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Gln
				500					505					510
Cys	Gly	Lys	Ala	Phe	Ile	Arg	Ala	Ser	Ser	Cys	Arg	Glu	His	Glu
				515					520					525
Arg	Thr	His	Thr	Ile	Asn	Arg								
				530										

<210> 27

<211> 444

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1395322CD1

<400> 27

Met	Glu	Arg	Tyr	Leu	Ser	Thr	Thr	Pro	Glu	Thr	Thr	His	Cys	Arg
1				5					10					15
Lys	Gln	Pro	Arg	Pro	Val	Arg	Ile	Gln	Thr	Leu	Val	Gly	Asn	Ile
				20					25					30
His	Ile	Lys	Gln	Glu	Met	Glu	Asp	Asp	Tyr	Asp	Tyr	Tyr	Gly	Gln
				35					40					45
Gln	Arg	Val	Gln	Ile	Leu	Glu	Arg	Asn	Glu	Ser	Glu	Glu	Cys	Thr
				50					55					60
Glu	Asp	Thr	Asp	Gln	Ala	Glu	Gly	Thr	Glu	Ser	Glu	Pro	Lys	Gly
				65					70					75
Glu	Ser	Phe	Asp	Ser	Gly	Val	Ser	Ser	Ser	Ile	Gly	Thr	Glu	Pro
				80					85					90
Asp	Ser	Val	Glu	Gln	Gln	Phe	Gly	Pro	Gly	Ala	Ala	Arg	Asp	Ser
				95					100					105
Gln	Ala	Glu	Pro	Thr	Gln	Pro	Glu	Gln	Ala	Ala	Glu	Ala	Pro	Ala
				110					115					120
Glu	Gly	Gly	Pro	Gln	Thr	Asn	Gln	Leu	Glu	Thr	Gly	Ala	Ser	Ser
				125					130					135
Pro	Glu	Arg	Ser	Asn	Glu	Val	Glu	Met	Asp	Ser	Thr	Val	Ile	Thr
				140					145					150
Val	Ser	Asn	Ser	Ser	Asp	Lys	Ser	Val	Leu	Gln	Gln	Pro	Ser	Val
				155					160					165
Asn	Thr	Ser	Ile	Gly	Gln	Pro	Leu	Pro	Ser	Thr	Gln	Leu	Tyr	Leu
				170					175					180
Arg	Gln	Thr	Glu	Thr	Leu	Thr	Ser	Asn	Leu	Arg	Met	Pro	Leu	Thr
				185					190					195
Leu	Thr	Ser	Asn	Thr	Gln	Val	Ile	Gly	Thr	Ala	Gly	Asn	Thr	Tyr
				200					205					210
Leu	Pro	Ala	Leu	Phe	Thr	Thr	Gln	Pro	Ala	Gly	Ser	Gly	Pro	Lys
				215					220					225
Pro	Phe	Leu	Phe	Ser	Leu	Pro	Gln	Pro	Leu	Ala	Gly	Gln	Gln	Thr
				230					235					240
Gln	Phe	Val	Thr	Val	Ser	Gln	Pro	Gly	Leu	Ser	Thr	Phe	Thr	Ala
				245					250					255
Gln	Leu	Pro	Ala	Pro	Gln	Pro	Leu	Ala	Ser	Ser	Ala	Gly	His	Ser
				260					265					270
Thr	Ala	Ser	Gly	Gln	Gly	Glu	Lys	Lys	Pro	Tyr	Glu	Cys	Thr	Leu
				275					280					285
Cys	Asn	Lys	Thr	Phe	Thr	Ala	Lys	Gln	Asn	Tyr	Val	Lys	His	Met
				290					295					300
Phe	Val	His	Thr	Gly	Glu	Lys	Pro	His	Gln	Cys	Ser	Ile	Cys	Trp
				305					310					315
Arg	Ser	Phe	Ser	Leu	Lys	Asp	Tyr	Leu	Ile	Lys	Leu	Met	Val	Thr
				320					325					330
His	Thr	Gly	Val	Arg	Ala	Tyr	Gln	Cys	Ser	Ile	Cys	Asn	Lys	Arg
				335					340					345
Phe	Thr	Gln	Lys	Ser	Ser	Leu	Asn	Val	His	Met	Arg	Leu	His	Arg
				350					355					360
Gly	Glu	Lys	Ser	Tyr	Glu	Cys	Tyr	Ile	Cys	Lys	Lys	Lys	Phe	Ser
				365					370					375
His	Lys	Thr	Leu	Leu	Glu	Arg	His	Val	Ala	Leu	His	Ser	Ala	Ser
				380					385					390
Asn	Gly	Thr	Pro	Pro	Ala	Gly	Thr	Pro	Pro	Gly	Ala	Arg	Ala	Gly
				395					400					405
Pro	Pro	Gly	Val	Val	Ala	Cys	Thr	Glu	Gly	Thr	Thr	Tyr	Val	Cys
				410					415					420
Ser	Val	Cys	Pro	Ala	Lys	Phe	Asp	Gln	Ile	Glu	Gln	Phe	Asn	Asp
				425					430					435
His	Met	Arg	Met	His	Val	Ser	Asp	Gly						
				440										

<210> 28

<211> 347

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1419370CD1

<400> 28

Met	Ser	Phe	Val	Leu	Ser	Arg	Met	Ala	Ala	Cys	Gly	Gly	Thr	Cys
1				5					10					15
Lys	Asn	Lys	Val	Thr	Val	Ser	Lys	Pro	Val	Trp	Asp	Phe	Leu	Ser
				20					25					30
Lys	Glu	Thr	Pro	Ala	Arg	Leu	Ala	Arg	Leu	Arg	Glu	Glu	His	Arg
				35					40					45
Val	Ser	Ile	Leu	Ile	Asp	Gly	Glu	Thr	Ser	Asp	Ile	Tyr	Val	Leu
				50					55					60
Gln	Leu	Ser	Pro	Gln	Gly	Pro	Pro	Pro	Ala	Pro	Pro	Asn	Gly	Leu
				65					70					75
Tyr	Leu	Ala	Arg	Lys	Ala	Leu	Lys	Gly	Leu	Leu	Lys	Glu	Ala	Glu
				80					85					90
Lys	Glu	Leu	Lys	Lys	Ala	Gln	Arg	Gln	Gly	Glu	Leu	Met	Gly	Cys
				95					100					105
Leu	Ala	Leu	Gly	Gly	Gly	Glu	His	Pro	Glu	Met	His	Arg	Ala	
				110					115					120
Gly	Pro	Pro	Pro	Leu	Arg	Ala	Ala	Pro	Leu	Leu	Pro	Pro	Gly	Ala
				125					130					135
Arg	Gly	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Pro	Leu	Pro
				140					145					150
Pro	Arg	Leu	Arg	Glu	Glu	Ala	Glu	Glu	Gln	Glu	Ser	Thr	Cys	Pro
				155					160					165
Ile	Cys	Leu	Gly	Glu	Ile	Gln	Asn	Ala	Lys	Thr	Leu	Glu	Lys	Cys
				170					175					180
Arg	His	Ser	Phe	Cys	Glu	Gly	Cys	Ile	Thr	Arg	Ala	Leu	Gln	Val
				185					190					195
Lys	Lys	Ala	Cys	Pro	Met	Cys	Gly	Arg	Phe	Tyr	Gly	Gln	Leu	Val
				200					205					210
Gly	Asn	Gln	Pro	Gln	Asn	Gly	Arg	Met	Leu	Val	Ser	Lys	Asp	Ala
				215					220					225
Thr	Leu	Leu	Leu	Pro	Ser	Tyr	Glu	Lys	Tyr	Gly	Thr	Ile	Val	Ile
				230					235					240
Gln	Tyr	Val	Phe	Pro	Pro	Gly	Val	Gln	Gly	Ala	Glu	His	Pro	Asn
				245					250					255
Pro	Gly	Val	Arg	Tyr	Pro	Gly	Thr	Thr	Arg	Val	Ala	Tyr	Leu	Pro
				260					265					270
Asp	Cys	Pro	Glu	Gly	Asn	Lys	Val	Leu	Thr	Leu	Phe	Arg	Lys	Ala
				275					280					285
Phe	Asp	Gln	Arg	Leu	Thr	Phe	Thr	Ile	Gly	Thr	Ser	Met	Thr	Thr
				290					295					300
Gly	Arg	Pro	Asn	Val	Ile	Thr	Trp	Asn	Asp	Ile	His	His	Lys	Thr
				305					310					315
Ser	Cys	Thr	Gly	Gly	Pro	Gln	Leu	Phe	Gly	Tyr	Pro	Asp	Pro	Thr
				320					325					330
Tyr	Leu	Thr	Arg	Val	Gln	Glu	Glu	Leu	Arg	Ala	Lys	Gly	Ile	Thr
				335					340					345

Asp Asp

<210> 29

<211> 308

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1429773CD1

<400> 29

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Met Gln Pro Ser Gly His Arg Leu Arg Asp Val Glu His His Pro
 1          5          10          15
Leu Leu Ala Glu Asn Asp Asn Tyr Asp Ser Ser Ser Ser Ser
          20          25          30
Ser Glu Ala Asp Val Ala Asp Arg Val Trp Phe Ile Arg Asp Gly
          35          40          45
Cys Gly Met Ile Cys Ala Val Met Thr Trp Leu Leu Val Ala Tyr
          50          55          60
Ala Asp Phe Val Val Thr Phe Val Met Leu Leu Pro Ser Lys Asp
          65          70          75
Phe Trp Tyr Ser Val Val Asn Gly Val Ile Phe Asn Cys Leu Ala
          80          85          90
Val Leu Ala Leu Ser Ser His Leu Arg Thr Met Leu Thr Asp Pro
          95          100          105
Gly Ala Val Pro Lys Gly Asn Ala Thr Lys Glu Tyr Met Glu Ser
          110          115          120
Leu Gln Leu Lys Pro Gly Glu Val Ile Tyr Lys Cys Pro Lys Cys
          125          130          135
Cys Cys Ile Lys Pro Glu Arg Ala His His Cys Ser Ile Cys Lys
          140          145          150
Arg Cys Ile Arg Lys Met Asp His His Cys Pro Trp Val Asn Asn
          155          160          165
Cys Val Gly Glu Lys Asn Gln Arg Phe Phe Val Leu Phe Thr Met
          170          175          180
Tyr Ile Ala Leu Ser Ser Val His Ala Leu Ile Leu Cys Gly Phe
          185          190          195
Gln Phe Ile Ser Cys Val Arg Gly Gln Trp Thr Glu Cys Ser Asp
          200          205          210
Phe Ser Pro Pro Ile Thr Val Ile Leu Leu Ile Phe Leu Cys Leu
          215          220          225
Glu Gly Leu Leu Phe Phe Thr Phe Thr Ala Val Met Phe Gly Thr
          230          235          240
Gln Ile His Ser Ile Cys Asn Asp Glu Thr Glu Ile Glu Arg Leu
          245          250          255
Lys Ser Glu Lys Pro Thr Trp Glu Arg Arg Leu Arg Trp Glu Gly
          260          265          270
Met Lys Ser Val Phe Gly Gly Pro Pro Ser Leu Leu Trp Met Asn
          275          280          285
Pro Phe Val Gly Phe Arg Phe Arg Arg Leu Pro Thr Arg Pro Arg
          290          295          300
Lys Gly Gly Pro Glu Phe Ser Val
          305

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<210> 30

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1470820CD1

<400> 30

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Met Cys Tyr Ile Tyr Pro Phe Val Phe Leu Arg Leu Asp Ser Met
 1          5          10          15
Lys Glu Leu His Lys Thr Asn Arg Gln Gln His Glu Lys His Leu
          20          25          30
Gln Ser Arg Val Asp Ser Thr Arg Ala Ile Glu Arg Leu Glu Gly

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				35					40				45	
Ser	Ser	Gly	Gly	Ile	Gly	Glu	Arg	Tyr	Lys	Phe	Leu	Gln	Glu	Met
				50					55					60
Arg	Gly	Tyr	Val	Gln	Asp	Leu	Leu	Glu	Cys	Phe	Ser	Glu	Lys	Val
				65					70					75
Arg	Met	Gln	Lys	Tyr										
				80										

<210> 31

<211> 570

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1483455CD1

<400> 31

Met	Pro	Gln	Val	Thr	Phe	Asn	Asp	Val	Ala	Ile	Asp	Phe	Thr	His
1				5					10					15
Glu	Glu	Trp	Gly	Trp	Leu	Ser	Ser	Ala	Gln	Arg	Asp	Leu	Tyr	Lys
				20					25					30
Asp	Val	Met	Val	Gln	Asn	Tyr	Glu	Asn	Leu	Val	Ser	Val	Gly	Leu
				35					40					45
Ser	Val	Thr	Lys	Pro	Tyr	Val	Ile	Thr	Leu	Leu	Glu	Asp	Gly	Lys
				50					55					60
Glu	Pro	Trp	Met	Met	Glu	Lys	Lys	Leu	Ser	Lys	Gly	Met	Ile	Pro
				65					70					75
Asp	Trp	Glu	Ser	Arg	Trp	Glu	Asn	Lys	Glu	Leu	Ser	Thr	Lys	Lys
				80					85					90
Asp	Asn	Tyr	Asp	Glu	Asp	Ser	Pro	Gln	Thr	Val	Ile	Ile	Glu	Lys
				95					100					105
Val	Val	Lys	Gln	Ser	Tyr	Glu	Phe	Ser	Asn	Ser	Lys	Lys	Asn	Leu
				110					115					120
Glu	Tyr	Ile	Glu	Lys	Leu	Glu	Gly	Lys	His	Gly	Ser	Gln	Val	Asp
				125					130					135
His	Phe	Arg	Pro	Ala	Ile	Leu	Thr	Ser	Arg	Glu	Ser	Pro	Thr	Ala
				140					145					150
Asp	Ser	Val	Tyr	Lys	Tyr	Asn	Ile	Phe	Arg	Ser	Thr	Phe	His	Ser
				155					160					165
Lys	Ser	Thr	Leu	Ser	Glu	Pro	Gln	Lys	Ile	Ser	Ala	Glu	Gly	Asn
				170					175					180
Ser	His	Lys	Tyr	Asp	Ile	Leu	Lys	Lys	Asn	Leu	Pro	Lys	Lys	Ser
				185					190					195
Val	Ile	Lys	Asn	Glu	Lys	Val	Asn	Gly	Gly	Lys	Lys	Leu	Leu	Asn
				200					205					210
Ser	Asn	Lys	Ser	Gly	Ala	Ala	Phe	Ser	Gln	Gly	Lys	Ser	Leu	Thr
				215					220					225
Leu	Pro	Gln	Thr	Cys	Asn	Arg	Glu	Lys	Ile	Tyr	Thr	Cys	Ser	Glu
				230					235					240
Cys	Gly	Lys	Ala	Phe	Gly	Lys	Gln	Ser	Ile	Leu	Asn	Arg	His	Trp
				245					250					255
Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Arg	Glu	Cys	Gly
				260					265					270
Lys	Thr	Phe	Ser	His	Gly	Ser	Ser	Leu	Thr	Arg	His	Leu	Ile	Ser
				275					280					285
His	Ser	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Ile	Glu	Cys	Gly	Lys	Ala
				290					295					300
Phe	Ser	His	Val	Ser	Ser	Leu	Thr	Asn	His	Gln	Ser	Thr	His	Thr
				305					310					315
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Met	Asn	Cys	Gly	Lys	Ser	Phe	Ser
				320					325					330
Arg	Val	Ser	His	Leu	Ile	Glu	His	Leu	Arg	Ile	His	Thr	Gln	Glu

	335		340		345
Lys Leu Tyr Glu	Cys Arg Ile Cys Gly	Lys Ala Phe Ile His	Arg		
	350		355		360
Ser Ser Leu Ile	His His Gln Lys Ile	His Thr Gly Glu Lys	Pro		
	365		370		375
Tyr Glu Cys Arg	Glu Cys Gly Lys Ala Phe	Cys Cys Ser Ser	His		
	380		385		390
Leu Thr Arg His	Gln Arg Ile His Thr	Met Glu Lys Gln Tyr	Glu		
	395		400		405
Cys Asn Lys Cys	Leu Lys Val Phe Ser	Ser Leu Ser Phe Leu	Val		
	410		415		420
Gln His Gln Ser	Ile His Thr Glu Glu	Lys Pro Phe Glu Cys	Gln		
	425		430		435
Lys Cys Arg Lys	Ser Phe Asn Gln Leu	Glu Ser Leu Asn Met	His		
	440		445		450
Leu Arg Asn His	Ile Arg Leu Lys Pro	Tyr Glu Cys Ser Ile	Cys		
	455		460		465
Gly Lys Ala Phe	Ser His Arg Ser Ser	Leu Leu Gln His His	Arg		
	470		475		480
Ile His Thr Gly	Glu Lys Pro Tyr Glu	Cys Ile Lys Cys Gly	Lys		
	485		490		495
Thr Phe Ser Cys	Ser Ser Asn Leu Thr	Val His Gln Arg Ile	His		
	500		505		510
Thr Gly Glu Lys	Pro Tyr Lys Cys Asn	Glu Cys Gly Lys Ala	Phe		
	515		520		525
Ser Lys Gly Ser	Asn Leu Thr Ala His	Gln Arg Val His Asn	Gly		
	530		535		540
Glu Lys Pro Asn	Ser Val Val Ser Val	Glu Lys Pro Leu Asp	Tyr		
	545		550		555
Met Asn His Tyr	Thr Cys Glu Lys Ser	Tyr Arg Arg Glu Thr	Val		
	560		565		570

<210> 32

<211> 390

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1527064CD1

<400> 32

Met Arg Gly Asp Arg	Gly Arg Gly Arg	Gly Gly Arg Phe Gly	Ser
1	5	10	15
Arg Gly Gly Pro Gly	Gly Gly Phe Arg	Pro Phe Val Pro His	Ile
	20	25	30
Pro Phe Asp Phe Tyr	Leu Cys Glu Met	Ala Phe Pro Arg Val	Lys
	35	40	45
Pro Ala Pro Asp Glu	Thr Ser Phe Ser	Glu Ala Leu Leu Lys	Arg
	50	55	60
Asn Gln Asp Leu Ala	Pro Asn Ser Ala	Glu Gln Ala Ser Ile	Leu
	65	70	75
Ser Leu Val Thr Lys	Ile Asn Asn Val	Ile Asp Asn Leu Ile	Val
	80	85	90
Ala Pro Gly Thr Phe	Glu Val Gln Ile	Glu Glu Val Arg Gln	Val
	95	100	105
Gly Ser Tyr Lys Lys	Gly Thr Met Thr	Thr Gly His Asn Val	Ala
	110	115	120
Asp Leu Val Val Ile	Leu Lys Ile Leu	Pro Thr Leu Glu Ala	Val
	125	130	135
Ala Ala Leu Gly Asn	Lys Val Val Glu	Ser Leu Arg Ala Gln	Asp
	140	145	150

Pro	Ser	Glu	Val	Leu	Thr	Met	Leu	Thr	Asn	Glu	Thr	Gly	Phe	Glu
				155					160					165
Ile	Ser	Ser	Ser	Asp	Ala	Thr	Val	Lys	Ile	Leu	Ile	Thr	Thr	Val
				170					175					180
Pro	Pro	Asn	Leu	Arg	Lys	Leu	Asp	Pro	Glu	Leu	His	Leu	Asp	Ile
				185					190					195
Lys	Val	Leu	Gln	Ser	Ala	Leu	Ala	Ala	Ile	Arg	His	Ala	Arg	Trp
				200					205					210
Phe	Glu	Glu	Asn	Ala	Ser	Gln	Ser	Thr	Val	Lys	Val	Leu	Ile	Arg
				215					220					225
Leu	Leu	Lys	Asp	Leu	Arg	Ile	Arg	Phe	Pro	Gly	Phe	Glu	Pro	Leu
				230					235					240
Thr	Pro	Trp	Ile	Leu	Asp	Leu	Leu	Gly	His	Tyr	Ala	Val	Met	Asn
				245					250					255
Asn	Pro	Thr	Arg	Gln	Pro	Leu	Ala	Leu	Asn	Val	Ala	Tyr	Arg	Arg
				260					265					270
Cys	Leu	Gln	Ile	Leu	Ala	Ala	Gly	Leu	Phe	Leu	Pro	Gly	Ser	Val
				275					280					285
Gly	Ile	Thr	Asp	Pro	Cys	Glu	Ser	Gly	Asn	Phe	Arg	Val	His	Thr
				290					295					300
Val	Met	Thr	Leu	Glu	Gln	Gln	Asp	Met	Val	Cys	Tyr	Thr	Ala	Gln
				305					310					315
Thr	Leu	Val	Arg	Ile	Leu	Ser	His	Gly	Gly	Phe	Arg	Lys	Ile	Leu
				320					325					330
Gly	Gln	Glu	Gly	Asp	Ala	Ser	Tyr	Leu	Ala	Ser	Glu	Ile	Ser	Thr
				335					340					345
Trp	Asp	Gly	Val	Ile	Val	Thr	Pro	Ser	Glu	Lys	Ala	Tyr	Glu	Lys
				350					355					360
Pro	Pro	Glu	Lys	Lys	Glu	Gly	Glu	Glu	Glu	Glu	Glu	Asn	Thr	Glu
				365					370					375
Glu	Pro	Pro	Gln	Gly	Glu	Glu	Glu	Glu	Ser	Met	Glu	Thr	Gln	Glu
				380					385					390

<210> 33

<211> 601

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1557491CD1

<400> 33

Met	Asn	Glu	Ser	Ala	Pro	Gly	Thr	Tyr	Val	Val	Gln	Asn	Pro	His
1				5					10					15
Ser	Ser	Glu	Leu	Pro	Thr	Leu	Asn	Phe	Gln	Asp	Thr	Val	Asn	Thr
				20					25					30
Leu	Thr	Asn	Ser	Pro	Ala	Ile	Pro	Leu	Glu	Thr	Ser	Ala	Cys	Gln
				35					40					45
Asp	Ile	Pro	Thr	Ser	Ala	Asn	Val	Gln	Asn	Ala	Glu	Gly	Thr	Lys
				50					55					60
Trp	Gly	Glu	Glu	Ala	Leu	Lys	Met	Asp	Leu	Asp	Asn	Asn	Phe	Tyr
				65					70					75
Ser	Thr	Glu	Val	Ser	Val	Ser	Ser	Thr	Glu	Asn	Ala	Val	Ser	Ser
				80					85					90
Asp	Leu	Arg	Ala	Gly	Asp	Val	Pro	Val	Leu	Ser	Leu	Ser	Asn	Ser
				95					100					105
Ser	Glu	Asn	Ala	Ala	Ser	Val	Ile	Ser	Tyr	Ser	Gly	Ser	Ala	Pro
				110					115					120
Ser	Val	Ile	Val	His	Ser	Ser	Gln	Phe	Ser	Ser	Val	Ile	Met	His
				125					130					135
Ser	Asn	Ala	Ile	Ala	Ala	Met	Thr	Ser	Ser	Asn	His	Arg	Ala	Phe

	140		145		150
Ser Asp Pro Ala	Val Ser Gln Ser Leu	Lys Asp Asp Ser Lys	Pro		
	155		160		165
Glu Pro Asp Lys	Val Gly Arg Phe Ala	Ser Arg Pro Lys Ser	Ile		
	170		175		180
Lys Glu Lys Lys	Lys Thr Thr Ser His	Thr Arg Gly Glu Ile	Pro		
	185		190		195
Glu Glu Ser Asn	Tyr Val Ala Asp Pro	Gly Gly Ser Leu Ser	Lys		
	200		205		210
Thr Thr Asn Ile	Ala Glu Glu Thr Ser	Lys Ile Glu Thr Tyr	Ile		
	215		220		225
Ala Lys Pro Ala	Leu Pro Gly Thr Ser	Thr Asn Ser Asn Val	Ala		
	230		235		240
Pro Leu Cys Gln	Ile Thr Val Lys Ile	Gly Asn Glu Ala Ile	Val		
	245		250		255
Lys Arg His Ile	Leu Gly Ser Lys Leu	Phe Tyr Lys Arg Gly	Arg		
	260		265		270
Arg Pro Lys Tyr	Gln Met Gln Glu Glu	Pro Leu Pro Gln Gly	Asn		
	275		280		285
Asp Pro Glu Pro	Ser Gly Asp Ser Pro	Leu Gly Leu Cys Gln	Ser		
	290		295		300
Glu Cys Met Glu	Met Ser Glu Val Phe	Asp Asp Ala Ser Asp	Gln		
	305		310		315
Asp Ser Thr Asp	Lys Pro Trp Arg Pro	Tyr Tyr Asn Tyr Lys	Pro		
	320		325		330
Lys Lys Lys Ser	Arg Gln Leu Lys Lys	Met Arg Lys Val Asn	Trp		
	335		340		345
Arg Lys Glu His	Gly Asn Arg Ser Pro	Ser His Lys Cys Lys	Tyr		
	350		355		360
Pro Ala Glu Leu	Asp Cys Ala Val Gly	Lys Ala Pro Gln Asp	Lys		
	365		370		375
Pro Phe Glu Glu	Glu Glu Thr Lys Glu	Met Pro Lys Leu Gln	Cys		
	380		385		390
Glu Leu Cys Asp	Gly Asp Lys Ala Val	Gly Ala Gly Asn Gln	Gly		
	395		400		405
Arg Pro His Arg	His Leu Thr Ser Arg	Pro Tyr Ala Cys Glu	Leu		
	410		415		420
Cys Ala Lys Gln	Phe Gln Ser Pro Ser	Thr Leu Lys Met His	Met		
	425		430		435
Arg Cys His Thr	Gly Glu Lys Pro Tyr	Gln Cys Lys Thr Cys	Gly		
	440		445		450
Arg Cys Phe Ser	Val Gln Gly Asn Leu	Gln Lys His Glu Arg	Ile		
	455		460		465
His Leu Gly Leu	Lys Glu Phe Val Cys	Gln Tyr Cys Asn Lys	Ala		
	470		475		480
Phe Thr Leu Asn	Glu Thr Leu Lys Ile	His Glu Arg Ile His	Thr		
	485		490		495
Gly Glu Lys Arg	Tyr His Cys Gln Phe	Cys Phe Gln Arg Phe	Leu		
	500		505		510
Tyr Leu Ser Thr	Lys Arg Asn His Glu	Gln Arg His Ile Arg	Glu		
	515		520		525
His Asn Gly Lys	Gly Tyr Ala Cys Phe	Gln Cys Pro Lys Ile	Cys		
	530		535		540
Lys Thr Ala Ala	Ala Leu Gly Met His	Gln Lys Lys His Leu	Phe		
	545		550		555
Lys Ser Pro Ser	Gln Gln Glu Lys Ile	Gly Asp Val Cys His	Glu		
	560		565		570
Asn Ser Asn Pro	Leu Glu Asn Gln His	Phe Ile Gly Ser Glu	Asp		
	575		580		585
Asn Asp Gln Lys	Asp Asn Ile Gln Thr	Gly Val Glu Asn Val	Val		
	590		595		600
Leu					

<210> 34
 <211> 834
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1576862CD1

<400> 34

Met	Glu	Glu	Lys	Arg	Arg	Lys	Tyr	Ser	Ile	Ser	Ser	Asp	Asn	Ser	1	5	10	15
Asp	Thr	Thr	Asp	Ser	His	Ala	Thr	Ser	Thr	Ser	Ala	Ser	Arg	Cys	20	25	30	35
Ser	Lys	Leu	Pro	Ser	Ser	Thr	Lys	Ser	Gly	Trp	Pro	Arg	Gln	Asn	40	45	50	55
Glu	Lys	Lys	Pro	Ser	Glu	Val	Phe	Arg	Thr	Asp	Leu	Ile	Thr	Ala	60	65	70	75
Met	Lys	Ile	Pro	Asp	Ser	Tyr	Gln	Leu	Ser	Pro	Asp	Asp	Tyr	Tyr	80	85	90	95
Ile	Leu	Ala	Asp	Pro	Trp	Arg	Gln	Glu	Trp	Glu	Lys	Gly	Val	Gln	100	105	110	115
Val	Pro	Ala	Gly	Ala	Glu	Ala	Ile	Pro	Glu	Pro	Val	Val	Arg	Ile	120	125	130	135
Leu	Pro	Pro	Leu	Glu	Gly	Pro	Pro	Ala	Gln	Ala	Ser	Pro	Ser	Ser	140	145	150	155
Thr	Met	Leu	Gly	Glu	Gly	Ser	Gln	Pro	Asp	Trp	Pro	Gly	Gly	Ser	160	165	170	175
Arg	Tyr	Asp	Leu	Asp	Glu	Ile	Asp	Ala	Tyr	Trp	Leu	Glu	Leu	Ile	180	185	190	195
Asn	Ser	Glu	Leu	Lys	Glu	Met	Glu	Arg	Pro	Glu	Leu	Asp	Glu	Leu	200	205	210	215
Thr	Leu	Glu	Arg	Val	Leu	Glu	Glu	Leu	Glu	Thr	Leu	Cys	His	Gln	220	225	230	235
Asn	Met	Ala	Arg	Ala	Ile	Glu	Thr	Gln	Glu	Gly	Leu	Gly	Ile	Glu	240	245	250	255
Tyr	Asp	Glu	Asp	Val	Val	Cys	Asp	Val	Cys	Arg	Ser	Pro	Glu	Gly	260	265	270	275
Glu	Asp	Gly	Asn	Glu	Met	Val	Phe	Cys	Asp	Lys	Cys	Asn	Val	Cys	280	285	290	295
Val	His	Gln	Ala	Cys	Tyr	Gly	Ile	Leu	Lys	Val	Pro	Thr	Gly	Ser	300	305	310	315
Trp	Leu	Cys	Arg	Thr	Cys	Ala	Leu	Gly	Val	Gln	Pro	Lys	Cys	Leu	320	325	330	335
Leu	Cys	Pro	Lys	Arg	Gly	Gly	Ala	Leu	Lys	Pro	Thr	Arg	Ser	Gly	340	345	350	355
Thr	Lys	Trp	Val	His	Val	Ser	Cys	Ala	Leu	Trp	Ile	Pro	Glu	Val	360	365	370	375
Ser	Ile	Gly	Cys	Pro	Glu	Lys	Met	Glu	Pro	Ile	Thr	Lys	Ile	Ser	380	385	390	395
His	Ile	Pro	Ala	Ser	Arg	Trp	Ala	Leu	Ser	Cys	Ser	Leu	Cys	Lys	400	405	410	415
Glu	Cys	Thr	Gly	Thr	Cys	Ile	Gln	Cys	Ser	Met	Pro	Ser	Cys	Val	420	425	430	435
Thr	Ala	Phe	His	Val	Thr	Cys	Ala	Phe	Asp	His	Gly	Leu	Glu	Met	440	445	450	455
Arg	Thr	Ile	Leu	Ala	Asp	Asn	Asp	Glu	Val	Lys	Phe	Lys	Ser	Phe	460	465	470	475
Cys	Gln	Glu	His	Ser	Asp	Gly	Gly	Pro	Arg	Asn	Glu	Pro	Thr	Ser	480	485	490	495
Glu	Pro	Thr	Glu	Pro	Ser	Gln	Ala	Gly	Glu	Asp	Leu	Glu	Lys	Val	500	505	510	515
Thr	Leu	Arg	Lys	Gln	Arg	Leu	Gln	Gln	Leu	Glu	Glu	Asp	Phe	Tyr	520	525	530	535

	395		400		405
Glu Leu Val Glu	Pro Ala Glu Val Ala	Glu Arg Leu Asp Leu	Ala		
	410		415		420
Glu Ala Leu Val	Asp Phe Ile Tyr Gln	Tyr Trp Lys Leu Lys	Arg		
	425		430		435
Lys Ala Asn Ala	Asn Gln Pro Leu Leu	Thr Pro Lys Thr Asp	Glu		
	440		445		450
Val Asp Asn Leu	Ala Gln Gln Glu Gln	Asp Val Leu Tyr Arg	Arg		
	455		460		465
Leu Lys Leu Phe	Thr His Leu Arg Gln	Asp Leu Glu Arg Val	Arg		
	470		475		480
Asn Leu Cys Tyr	Met Val Thr Arg Arg	Glu Arg Thr Lys His	Ala		
	485		490		495
Ile Cys Lys Leu	Gln Glu Gln Ile Phe	His Leu Gln Met Lys	Leu		
	500		505		510
Ile Glu Gln Asp	Leu Cys Arg Glu Arg	Ser Gly Arg Arg Ala	Lys		
	515		520		525
Gly Lys Lys Ser	Asp Ser Lys Arg Lys	Gly Cys Glu Gly Ser	Lys		
	530		535		540
Gly Ser Thr Glu	Lys Lys Glu Lys Val	Lys Ala Gly Pro Asp	Ser		
	545		550		555
Val Leu Gly Gln	Leu Ala Gly Leu Ser	Thr Ser Phe Pro Ile	Asp		
	560		565		570
Gly Thr Phe Phe	Asn Ser Trp Leu Ala	Gln Ser Val Gln Ile	Thr		
	575		580		585
Ala Glu Asn Met	Ala Met Ser Glu Trp	Pro Leu Asn Asn Gly	His		
	590		595		600
Arg Glu Asp Pro	Ala Pro Gly Leu Leu	Ser Glu Glu Leu Leu	Gln		
	605		610		615
Asp Glu Glu Thr	Leu Leu Ser Phe Met	Arg Asp Pro Ser Leu	Arg		
	620		625		630
Pro Gly Asp Pro	Ala Arg Lys Ala Arg	Gly Arg Thr Arg Leu	Pro		
	635		640		645
Ala Lys Lys Lys	Pro Pro Pro Pro	Pro Gln Asp Gly Pro	Gly		
	650		655		660
Ser Arg Thr Thr	Pro Asp Lys Ala Pro	Lys Lys Thr Trp Gly	Gln		
	665		670		675
Asp Ala Gly Ser	Gly Lys Gly Gly Gln	Gly Pro Pro Thr Arg	Lys		
	680		685		690
Pro Pro Arg Arg	Thr Ser Ser His Leu	Pro Ser Ser Pro Ala	Ala		
	695		700		705
Gly Asp Cys Pro	Ile Leu Ala Thr Pro	Glu Ser Pro Pro Pro	Leu		
	710		715		720
Ala Pro Glu Thr	Pro Asp Glu Ala Ala	Ser Val Ala Ala Asp	Ser		
	725		730		735
Asp Val Gln Val	Pro Gly Pro Ala Ala	Ser Pro Lys Pro Leu	Gly		
	740		745		750
Arg Leu Arg Pro	Pro Arg Glu Ser Lys	Val Thr Arg Arg Leu	Pro		
	755		760		765
Gly Ala Arg Pro	Asp Ala Gly Met Gly	Pro Pro Ser Ala Val	Ala		
	770		775		780
Glu Arg Pro Lys	Val Ser Leu His Phe	Asp Thr Glu Thr Asp	Gly		
	785		790		795
Tyr Phe Ser Asp	Gly Glu Met Ser Asp	Ser Asp Val Glu Ala	Glu		
	800		805		810
Asp Gly Gly Val	Gln Arg Gly Pro Arg	Glu Ala Gly Ala Glu	Glu		
	815		820		825
Val Val Arg Met	Gly Val Leu Ala Ser				
	830				

<210> 35
 <211> 499
 <212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1609731CD1

<400> 35

Met	Ala	Gln	Gly	Leu	Val	Thr	Phe	Arg	Asp	Val	Ala	Ile	Glu	Phe
1				5					10					15
Ser	Leu	Glu	Glu	Trp	Lys	Cys	Leu	Glu	Pro	Ala	Gln	Arg	Asp	Leu
				20					25					30
Tyr	Arg	Glu	Val	Thr	Leu	Glu	Asn	Phe	Gly	His	Leu	Ala	Ser	Leu
				35					40					45
Gly	Leu	Ser	Ile	Ser	Lys	Pro	Asp	Val	Val	Ser	Leu	Leu	Glu	Gln
				50					55					60
Gly	Lys	Glu	Pro	Trp	Met	Ile	Ala	Asn	Asp	Val	Thr	Gly	Pro	Trp
				65					70					75
Cys	Pro	Asp	Leu	Glu	Ser	Arg	Cys	Glu	Lys	Phe	Leu	Gln	Lys	Asp
				80					85					90
Ile	Phe	Glu	Ile	Gly	Ala	Phe	Asn	Trp	Glu	Ile	Met	Glu	Ser	Leu
				95					100					105
Lys	Cys	Ser	Asp	Leu	Glu	Gly	Ser	Asp	Phe	Arg	Ala	Asp	Trp	Glu
				110					115					120
Cys	Glu	Gly	Gln	Phe	Glu	Arg	Gln	Val	Asn	Glu	Glu	Cys	Tyr	Phe
				125					130					135
Lys	Gln	Val	Asn	Val	Thr	Tyr	Gly	His	Met	Pro	Val	Phe	Gln	His
				140					145					150
His	Thr	Ser	His	Thr	Val	Arg	Gln	Ser	Arg	Glu	Thr	Gly	Glu	Lys
				155					160					165
Leu	Met	Glu	Cys	His	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Arg	Gly	Ser
				170					175					180
His	Leu	Ile	Gln	His	Gln	Lys	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe
				185					190					195
Gly	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Arg	Ala	Ser	His	Leu
				200					205					210
Val	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Asp	Cys
				215					220					225
Lys	Asp	Cys	Gly	Lys	Ala	Phe	Gly	Arg	Thr	Ser	Glu	Leu	Ile	Leu
				230					235					240
His	Gln	Arg	Leu	His	Thr	Gly	Val	Lys	Pro	Tyr	Glu	Cys	Lys	Glu
				245					250					255
Cys	Gly	Lys	Thr	Phe	Arg	Gln	His	Ser	Gln	Leu	Ile	Leu	His	Gln
				260					265					270
Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Val	Cys	Lys	Asp	Cys	Gly
				275					280					285
Lys	Ala	Phe	Ile	Arg	Gly	Ser	Gln	Leu	Thr	Val	His	Arg	Arg	Ile
				290					295					300
His	Thr	Gly	Ala	Arg	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Ala
				305					310					315
Phe	Arg	Gln	His	Ser	Gln	Leu	Thr	Val	His	Gln	Arg	Ile	His	Thr
				320					325					330
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Gly	Phe	Ile
				335					340					345
His	Ser	Ser	Glu	Val	Thr	Arg	His	Gln	Arg	Asn	Ser	Phe	Trp	Gly
				350					355					360
Glu	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Arg	Gln	His
				365					370					375
Ala	Gln	Leu	Thr	Arg	His	Gln	Arg	Val	His	Thr	Gly	Asp	Arg	Pro
				380					385					390
Tyr	Glu	Cys	Lys	Asp	Cys	Gly	Lys	Ala	Phe	Ser	Arg	Ser	Ser	Tyr
				395					400					405
Leu	Ile	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Asp	Lys	Pro	Tyr	Glu
				410					415					420

Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Ile	Arg	Val	Ser	Gln	Leu	Thr	
				425					430					435	
His	His	Gln	Arg	Ile	His	Thr	Cys	Glu	Lys	Pro	Tyr	Glu	Cys	Arg	
				440					445					450	
Glu	Cys	Gly	Met	Ala	Phe	Ile	Arg	Ser	Ser	Gln	Leu	Thr	Glu	His	
				455					460					465	
Gln	Arg	Ile	His	Pro	Gly	Ile	Lys	Pro	Tyr	Glu	Cys	Arg	Glu	Cys	
				470					475					480	
Gly	Gln	Ala	Phe	Ile	Leu	Gly	Ser	Gln	Leu	Ile	Glu	His	Tyr	Arg	
				485					490					495	
Ile	His	Thr	Gly												

<210> 36
 <211> 402
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1674538CD1

<400> 36

Met	Tyr	Thr	Ser	Glu	Glu	Lys	Cys	Asn	Gln	Arg	Thr	Gln	Lys	Arg	
1				5					10					15	
Lys	Ile	Tyr	Asn	Val	Cys	Pro	Arg	Lys	Gly	Lys	Lys	Ile	Phe	Ile	
				20					25					30	
His	Met	His	Glu	Ile	Ile	Gln	Ile	Asp	Gly	His	Ile	Tyr	Gln	Cys	
				35					40					45	
Leu	Glu	Cys	Lys	Gln	Asn	Phe	Cys	Glu	Asn	Leu	Ala	Leu	Ile	Met	
				50					55					60	
Cys	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Asp	Met	
				65					70					75	
Cys	Glu	Lys	Thr	Phe	Val	Gln	Ser	Ser	Asp	Leu	Thr	Ser	His	Gln	
				80					85					90	
Arg	Ile	His	Asn	Tyr	Glu	Lys	Pro	Tyr	Lys	Cys	Ser	Lys	Cys	Glu	
				95					100					105	
Lys	Ser	Phe	Trp	His	His	Leu	Ala	Leu	Ser	Gly	His	Gln	Arg	Thr	
				110					115					120	
His	Ala	Gly	Lys	Lys	Phe	Tyr	Thr	Cys	Asp	Ile	Cys	Gly	Lys	Asn	
				125					130					135	
Phe	Gly	Gln	Ser	Ser	Asp	Leu	Leu	Val	His	Gln	Arg	Ser	His	Thr	
				140					145					150	
Gly	Glu	Lys	Pro	Tyr	Leu	Cys	Ser	Glu	Cys	Asp	Lys	Cys	Phe	Ser	
				155					160					165	
Arg	Ser	Thr	Asn	Leu	Ile	Arg	His	Arg	Arg	Thr	His	Thr	Gly	Glu	
				170					175					180	
Lys	Pro	Phe	Lys	Cys	Leu	Glu	Cys	Glu	Lys	Ala	Phe	Ser	Gly	Lys	
				185					190					195	
Ser	Asp	Leu	Ile	Ser	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Arg	Pro	
				200					205					210	
Tyr	Lys	Cys	Asn	Lys	Cys	Glu	Lys	Ser	Tyr	Arg	His	Arg	Ser	Ala	
				215					220					225	
Phe	Ile	Val	His	Lys	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	
				230					235					240	
Cys	Gly	Ala	Cys	Glu	Lys	Cys	Phe	Gly	Gln	Lys	Ser	Asp	Leu	Ile	
				245					250					255	
Val	His	Gln	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Leu	
				260					265					270	
Glu	Cys	Met	Arg	Ser	Phe	Thr	Arg	Ser	Ala	Asn	Leu	Ile	Arg	His	
				275					280					285	
Gln	Ala	Thr	His	Thr	His	Thr	Phe	Lys	Cys	Leu	Glu	Tyr	Glu	Lys	
				290					295					300	

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Ser Phe Asn Cys Ser Ser Asp Leu Ile Val His Gln Arg Ile His
305 310 315
Met Glu Glu Lys Pro His Gln Trp Ser Ala Cys Glu Ser Gly Phe
320 325 330
Leu Leu Gly Met Asp Phe Val Ala Gln Gln Lys Met Arg Thr Gln
335 340 345
Thr Glu Glu Leu His Tyr Lys Tyr Thr Val Cys Asp Lys Ser Phe
350 355 360
His Gln Ser Ser Ala Leu Leu Gln His Gln Thr Val His Ile Gly
365 370 375
Glu Lys Pro Phe Val Cys Asn Val Ser Glu Lys Gly Leu Glu Leu
380 385 390
Ser Pro Pro His Ala Ser Glu Ala Ser Gln Met Ser
395 400

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<210> 37
 <211> 579
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1675287CD1

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<400> 37
Met Ile Arg Glu Gly Glu Ala Ala Gly Ala Cys Pro Glu Glu Ile
1 5 10 15
Phe Ser Ala Leu Gln Tyr Ser Gly Thr Glu Val Pro Leu Gln Trp
20 25 30
Leu Arg Ser Glu Leu Pro Tyr Val Leu Glu Met Val Ala Glu Leu
35 40 45
Ala Gly Gln Gln Asp Pro Gly Leu Gly Ala Phe Ser Cys Gln Glu
50 55 60
Ala Arg Arg Ala Trp Leu Asp Arg His Gly Asn Leu Asp Glu Ala
65 70 75
Val Glu Glu Cys Val Arg Thr Arg Arg Arg Lys Val Gln Glu Leu
80 85 90
Gln Ser Leu Gly Phe Gly Pro Glu Glu Gly Ser Leu Gln Ala Leu
95 100 105
Phe Gln His Gly Gly Asp Val Ser Arg Ala Leu Thr Glu Leu Gln
110 115 120
Arg Gln Arg Leu Glu Pro Phe Arg Gln Arg Leu Trp Asp Ser Gly
125 130 135
Pro Glu Pro Thr Pro Ser Trp Asp Gly Pro Asp Lys Gln Ser Leu
140 145 150
Val Arg Arg Leu Leu Ala Val Tyr Ala Leu Pro Ser Trp Gly Arg
155 160 165
Ala Glu Leu Ala Leu Ser Leu Leu Gln Glu Thr Pro Arg Asn Tyr
170 175 180
Glu Leu Gly Asp Val Val Glu Ala Val Arg His Ser Gln Asp Arg
185 190 195
Ala Phe Leu Arg Arg Leu Leu Ala Gln Glu Cys Ala Val Cys Gly
200 205 210
Trp Ala Leu Pro His Asn Arg Met Gln Ala Leu Thr Ser Cys Glu
215 220 225
Cys Thr Ile Cys Pro Asp Cys Phe Arg Gln His Phe Thr Ile Ala
230 235 240
Leu Lys Glu Lys His Ile Thr Asp Met Val Cys Pro Ala Cys Gly
245 250 255
Arg Pro Asp Leu Thr Asp Asp Thr Gln Leu Leu Ser Tyr Phe Ser
260 265 270
Thr Leu Asp Ile Gln Leu Arg Glu Ser Leu Glu Pro Asp Ala Tyr
275 280 285

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Ala	Leu	Phe	His	Lys	Lys	Leu	Thr	Glu	Gly	Val	Leu	Met	Arg	Asp	
				290					295					300	
Pro	Lys	Phe	Leu	Trp	Cys	Ala	Gln	Cys	Ser	Phe	Gly	Phe	Ile	Tyr	
				305					310					315	
Glu	Arg	Glu	Gln	Leu	Glu	Ala	Thr	Cys	Pro	Gln	Cys	His	Gln	Thr	
				320					325					330	
Phe	Cys	Val	Arg	Cys	Lys	Arg	Gln	Trp	Glu	Glu	Gln	His	Arg	Gly	
				335					340					345	
Arg	Ser	Cys	Glu	Asp	Phe	Gln	Asn	Trp	Lys	Arg	Met	Asn	Asp	Pro	
				350					355					360	
Glu	Tyr	Gln	Ala	Gln	Gly	Leu	Ala	Met	Tyr	Leu	Gln	Glu	Asn	Gly	
				365					370					375	
Ile	Asp	Cys	Pro	Lys	Cys	Lys	Phe	Ser	Tyr	Ala	Leu	Ala	Arg	Gly	
				380					385					390	
Gly	Cys	Met	His	Phe	His	Cys	Thr	Gln	Cys	Arg	His	Gln	Phe	Cys	
				395					400					405	
Ser	Gly	Cys	Tyr	Asn	Ala	Phe	Tyr	Ala	Lys	Asn	Lys	Cys	Pro	Glu	
				410					415					420	
Pro	Asn	Cys	Arg	Val	Lys	Lys	Ser	Leu	His	Gly	His	His	Pro	Arg	
				425					430					435	
Asp	Cys	Leu	Phe	Tyr	Leu	Arg	Asp	Trp	Thr	Ala	Leu	Arg	Leu	Gln	
				440					445					450	
Lys	Leu	Leu	Gln	Asp	Asn	Asn	Val	Met	Phe	Asn	Thr	Glu	Pro	Pro	
				455					460					465	
Ala	Gly	Ala	Arg	Ala	Val	Pro	Gly	Gly	Gly	Cys	Arg	Val	Ile	Glu	
				470					475					480	
Gln	Lys	Glu	Val	Pro	Asn	Gly	Leu	Arg	Asp	Glu	Ala	Cys	Gly	Lys	
				485					490					495	
Glu	Thr	Pro	Ala	Gly	Tyr	Ala	Gly	Leu	Cys	Gln	Ala	His	Tyr	Lys	
				500					505					510	
Glu	Tyr	Leu	Val	Ser	Leu	Ile	Asn	Ala	His	Ser	Leu	Asp	Pro	Ala	
				515					520					525	
Thr	Leu	Tyr	Glu	Val	Glu	Glu	Leu	Glu	Thr	Ala	Thr	Glu	Arg	Tyr	
				530					535					540	
Leu	His	Val	Arg	Pro	Gln	Pro	Leu	Ala	Gly	Glu	Asp	Pro	Pro	Ala	
				545					550					555	
Tyr	Gln	Ala	Arg	Leu	Leu	Gln	Lys	Leu	Thr	Glu	Glu	Val	Pro	Leu	
				560					565					570	
Gly	Gln	Ser	Ile	Pro	Arg	Arg	Arg	Lys							
				575											

<210> 38

<211> 426

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1693903CD1

<400> 38

Met	Pro	Pro	Lys	Lys	Gln	Ala	Gln	Ala	Gly	Gly	Ser	Lys	Lys	Ala	
1				5					10					15	
Glu	Gln	Lys	Lys	Lys	Glu	Lys	Ile	Ile	Glu	Asp	Lys	Thr	Phe	Gly	
				20					25					30	
Leu	Lys	Asn	Lys	Lys	Gly	Ala	Lys	Gln	Gln	Lys	Phe	Ile	Lys	Ala	
				35					40					45	
Val	Thr	His	Gln	Val	Lys	Phe	Gly	Gln	Gln	Asn	Pro	Arg	Gln	Val	
				50					55					60	
Ala	Gln	Ser	Glu	Ala	Glu	Lys	Lys	Leu	Lys	Lys	Asp	Asp	Lys	Lys	
				65					70					75	
Lys	Glu	Leu	Gln	Glu	Leu	Asn	Glu	Leu	Phe	Lys	Pro	Val	Val	Ala	
				80					85					90	

Ala	Gln	Lys	Ile	Ser	Lys	Gly	Ala	Asp	Pro	Lys	Ser	Val	Val	Cys	
				95					100					105	
Ala	Phe	Phe	Lys	Gln	Gly	Gln	Cys	Thr	Lys	Gly	Asp	Lys	Cys	Lys	
				110					115					120	
Phe	Ser	His	Asp	Leu	Thr	Leu	Glu	Arg	Lys	Cys	Glu	Lys	Arg	Ser	
				125					130					135	
Val	Tyr	Ile	Asp	Ala	Arg	Asp	Glu	Glu	Leu	Glu	Lys	Asp	Thr	Met	
				140					145					150	
Asp	Asn	Trp	Asp	Glu	Lys	Lys	Leu	Glu	Glu	Val	Val	Asn	Lys	Lys	
				155					160					165	
His	Gly	Glu	Ala	Glu	Lys	Lys	Lys	Pro	Lys	Thr	Gln	Ile	Val	Cys	
				170					175					180	
Lys	His	Phe	Leu	Glu	Ala	Ile	Glu	Asn	Asn	Lys	Tyr	Gly	Trp	Phe	
				185					190					195	
Trp	Val	Cys	Pro	Gly	Gly	Gly	Asp	Ile	Cys	Met	Tyr	Arg	His	Ala	
				200					205					210	
Leu	Pro	Pro	Gly	Phe	Val	Leu	Lys	Lys	Asp	Lys	Lys	Lys	Glu	Glu	
				215					220					225	
Lys	Glu	Asp	Glu	Ile	Ser	Leu	Glu	Asp	Leu	Ile	Glu	Arg	Glu	Arg	
				230					235					240	
Ser	Ala	Leu	Gly	Pro	Asn	Val	Thr	Lys	Ile	Thr	Leu	Glu	Ser	Phe	
				245					250					255	
Leu	Ala	Trp	Lys	Lys	Arg	Lys	Arg	Gln	Glu	Lys	Ile	Asp	Lys	Leu	
				260					265					270	
Glu	Gln	Asp	Met	Glu	Arg	Arg	Lys	Ala	Asp	Phe	Lys	Ala	Gly	Lys	
				275					280					285	
Ala	Leu	Val	Ile	Ser	Gly	Arg	Glu	Val	Phe	Glu	Phe	Arg	Pro	Glu	
				290					295					300	
Leu	Val	Asn	Asp	Asp	Asp	Glu	Glu	Ala	Asp	Asp	Thr	Arg	Tyr	Thr	
				305					310					315	
Gln	Gly	Thr	Gly	Gly	Asp	Glu	Val	Asp	Asp	Ser	Val	Ser	Val	Asn	
				320					325					330	
Asp	Ile	Asp	Leu	Ser	Leu	Tyr	Ile	Pro	Arg	Asp	Val	Asp	Glu	Thr	
				335					340					345	
Gly	Ile	Thr	Val	Ala	Ser	Leu	Glu	Arg	Phe	Ser	Thr	Tyr	Thr	Ser	
				350					355					360	
Asp	Lys	Asp	Glu	Asn	Lys	Leu	Ser	Glu	Ala	Ser	Gly	Gly	Arg	Ala	
				365					370					375	
Glu	Asn	Gly	Glu	Arg	Ser	Asp	Leu	Glu	Glu	Asp	Asn	Glu	Arg	Glu	
				380					385					390	
Gly	Thr	Glu	Asn	Gly	Ala	Ile	Asp	Ala	Val	Pro	Val	Asp	Glu	Asn	
				395					400					405	
Leu	Phe	Thr	Gly	Glu	Asp	Leu	Asp	Glu	Leu	Glu	Glu	Glu	Leu	Asn	
				410					415					420	
Thr	Leu	Asp	Leu	Glu	Glu										
				425											

<210> 39

<211> 266

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1702962CD1

<400> 39

Met	Gly	Ser	Lys	Thr	Leu	Pro	Ala	Pro	Val	Pro	Ile	His	Pro	Ser	
1				5					10					15	
Leu	Gln	Leu	Thr	Asn	Tyr	Ser	Phe	Leu	Gln	Ala	Val	Asn	Gly	Leu	
				20					25					30	
Pro	Thr	Val	Pro	Ser	Asp	His	Leu	Pro	Asn	Leu	Tyr	Gly	Phe	Ser	
				35					40					45	

Ala	Leu	His	Ala	Val	His	Leu	His	Gln	Trp	Thr	Leu	Gly	Tyr	Pro	
				50					55					60	
Ala	Met	His	Leu	Pro	Arg	Ser	Ser	Phe	Ser	Lys	Val	Pro	Gly	Thr	
				65					70					75	
Val	Ser	Ser	Leu	Val	Asp	Ala	Arg	Phe	Gln	Leu	Pro	Ala	Phe	Pro	
				80					85					90	
Trp	Phe	Pro	His	Val	Ile	Gln	Pro	Lys	Pro	Glu	Ile	Thr	Ala	Gly	
				95					100					105	
Gly	Ser	Val	Pro	Ala	Leu	Lys	Thr	Lys	Pro	Arg	Phe	Asp	Phe	Ala	
				110					115					120	
Asn	Leu	Ala	Leu	Ala	Ala	Thr	Gln	Glu	Asp	Pro	Ala	Lys	Leu	Gly	
				125					130					135	
Arg	Arg	Glu	Gly	Pro	Gly	Ser	Pro	Ala	Gly	Gly	Leu	Gly	Ala	Leu	
				140					145					150	
Leu	Asp	Val	Thr	Lys	Leu	Ser	Pro	Glu	Lys	Lys	Pro	Thr	Arg	Gly	
				155					160					165	
Arg	Leu	Pro	Ser	Lys	Thr	Lys	Lys	Glu	Phe	Val	Cys	Lys	Phe	Cys	
				170					175					180	
Gly	Arg	Gln	Phe	Thr	Lys	Ser	Tyr	Asn	Leu	Leu	Ile	His	Glu	Arg	
				185					190					195	
Thr	His	Thr	Asp	Glu	Arg	Pro	Tyr	Thr	Cys	Asp	Ile	Cys	His	Lys	
				200					205					210	
Ala	Phe	Arg	Arg	Gln	Asp	His	Leu	Arg	Asp	His	Arg	Tyr	Ile	His	
				215					220					225	
Ser	Lys	Glu	Lys	Pro	Phe	Lys	Cys	Gln	Glu	Cys	Gly	Lys	Gly	Phe	
				230					235					240	
Cys	Gln	Ser	Arg	Thr	Leu	Ala	Val	His	Lys	Thr	Leu	His	Ser	Gln	
				245					250					255	
Val	Lys	Glu	Leu	Lys	Thr	Ser	Lys	Ile	Lys	Cys					
				260					265						

<210> 40

<211> 358

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1712916CD1

<400> 40

Met	Asn	Thr	Ile	Val	Phe	Asn	Lys	Leu	Ser	Gly	Ala	Val	Leu	Phe	
1				5					10					15	
Glu	Asp	Gly	Gly	Ala	Ser	Glu	Arg	Glu	Arg	Gly	Gly	Arg	Pro	Tyr	
				20					25					30	
Ser	Gly	Val	Leu	Asp	Ser	Pro	His	Ala	Arg	Pro	Glu	Val	Gly	Ile	
				35					40					45	
Pro	Asp	Gly	Pro	Pro	Leu	Lys	Asp	Asn	Leu	Gly	Leu	Arg	His	Arg	
				50					55					60	
Arg	Thr	Gly	Ala	Arg	Gln	Asn	Gly	Gly	Lys	Val	Arg	His	Lys	Arg	
				65					70					75	
Gln	Ala	Leu	Gln	Asp	Met	Ala	Arg	Pro	Leu	Lys	Gln	Trp	Leu	Tyr	
				80					85					90	
Lys	His	Arg	Asp	Asn	Pro	Tyr	Pro	Thr	Lys	Thr	Glu	Lys	Ile	Leu	
				95					100					105	
Leu	Ala	Leu	Gly	Ser	Gln	Met	Thr	Leu	Val	Gln	Val	Ser	Asn	Trp	
				110					115					120	
Phe	Ala	Asn	Ala	Arg	Arg	Arg	Leu	Lys	Asn	Thr	Val	Arg	Gln	Pro	
				125					130					135	
Asp	Leu	Ser	Trp	Ala	Leu	Arg	Ile	Lys	Leu	Tyr	Asn	Lys	Tyr	Val	
				140					145					150	
Gln	Gly	Asn	Ala	Glu	Arg	Leu	Ser	Val	Ser	Ser	Asp	Asp	Ser	Cys	
				155					160					165	

Met	Met	Asp	Pro	Cys	Ser	Val	Gly	Val	Gln	Leu	Arg	Thr	Thr	Asn
1				5					10					15
Glu	Cys	His	Lys	Thr	Tyr	Tyr	Thr	Arg	His	Thr	Gly	Phe	Lys	Thr
				20					25					30
Leu	Gln	Glu	Leu	Ser	Ser	Asn	Asp	Met	Leu	Leu	Leu	Gln	Leu	Arg
				35					40					45
Thr	Gly	Met	Thr	Leu	Ser	Gly	Asn	Asn	Thr	Ile	Cys	Phe	His	His
				50					55					60
Val	Lys	Ile	Tyr	Ile	Asp	Arg	Phe	Glu	Asp	Leu	Gln	Lys	Ser	Cys
				65					70					75
Cys	Asp	Pro	Phe	Asn	Ile	His	Lys	Lys	Leu	Ala	Lys	Lys	Asn	Leu
				80					85					90
His	Val	Ile	Asp	Leu	Asp	Asp	Ala	Thr	Phe	Leu	Ser	Ala	Lys	Phe
				95					100					105
Gly	Arg	Gln	Leu	Val	Pro	Gly	Trp	Lys	Leu	Cys	Pro	Lys	Cys	Thr
				110					115					120
Gln	Ile	Ile	Asn	Gly	Ser	Val	Asp	Val	Asp	Thr	Glu	Asp	Arg	Gln
				125					130					135
Lys	Arg	Lys	Pro	Glu	Ser	Asp	Gly	Arg	Thr	Ala	Lys	Ala	Leu	Arg
				140					145					150
Ser	Leu	Gln	Phe	Thr	Asn	Pro	Gly	Arg	Gln	Thr	Glu	Phe	Ala	Pro
				155					160					165
Glu	Thr	Gly	Lys	Arg	Glu	Lys	Arg	Arg	Leu	Thr	Lys	Asn	Ala	Thr
				170					175					180
Ala	Gly	Ser	Asp	Arg	Gln	Val	Ile	Pro	Ala	Lys	Ser	Lys	Val	Tyr
				185					190					195

Asp	Ser	Gln	Gly	Leu	Leu	Ile	Phe	Ser	Gly	Met	Asp	Leu	Cys	Asp	
				200					205					210	
Cys	Leu	Asp	Glu	Asp	Cys	Leu	Gly	Cys	Phe	Tyr	Ala	Cys	Pro	Ala	
				215					220					225	
Cys	Gly	Ser	Thr	Lys	Cys	Gly	Ala	Glu	Cys	Arg	Cys	Asp	Arg	Lys	
				230					235					240	
Trp	Leu	Tyr	Glu	Gln	Ile	Glu	Ile	Glu	Gly	Gly	Glu	Ile	Ile	His	
				245					250					255	
Asn	Lys	His	Ala	Gly											
				260											

<210> 42

<211> 263

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1754833CD1

<400> 42

Met	Val	Leu	Pro	Pro	Pro	Gln	Leu	Pro	Gln	Thr	Arg	Ala	Gly	His	
1				5					10					15	
Arg	Trp	Ser	Thr	Trp	Thr	Ser	Thr	Cys	Ser	Arg	Cys	Arg	Arg	Ala	
				20					25					30	
Thr	Asp	Ser	Leu	Leu	Ser	Ala	Ser	Ser	Met	Thr	Ala	Ser	Arg	Ser	
				35					40					45	
Pro	Arg	Ser	Leu	Leu	Gly	Arg	Arg	Leu	Thr	Thr	Ala	Gly	Thr	Leu	
				50					55					60	
Arg	Ala	Gly	Gly	Arg	Glu	Thr	Ile	Arg	Pro	Gly	Thr	Gly	Thr	Ala	
				65					70					75	
Pro	Asp	Ser	Pro	Ala	Pro	Ala	Ser	Pro	Arg	Gly	Gly	Pro	Pro	Ala	
				80					85					90	
Gly	Thr	Lys	Ala	Ser	Pro	Arg	Trp	Lys	Gly	Ser	Ser	Ser	Ser	Ser	
				95					100					105	
Ser	Thr	Ala	Ser	Ser	Arg	Pro	Pro	Pro	Ser	Pro	Ala	Trp	Ala	Pro	
				110					115					120	
Trp	Gly	Val	Leu	His	Ser	Asn	Pro	Met	Asp	Tyr	Ala	Trp	Gly	Ala	
				125					130					135	
Asn	Gly	Leu	Asp	Ala	Ile	Ile	Thr	Gln	Leu	Leu	Asn	Gln	Phe	Glu	
				140					145					150	
Asn	Thr	Gly	Pro	Pro	Pro	Ala	Asp	Lys	Glu	Lys	Ile	Gln	Ala	Leu	
				155					160					165	
Pro	Thr	Val	Pro	Val	Thr	Glu	Glu	His	Val	Gly	Ser	Gly	Leu	Glu	
				170					175					180	
Cys	Pro	Val	Cys	Lys	Asp	Asp	Tyr	Ala	Leu	Gly	Glu	Arg	Val	Arg	
				185					190					195	
Gln	Leu	Pro	Cys	Asn	His	Leu	Phe	His	Asp	Gly	Cys	Ile	Val	Pro	
				200					205					210	
Trp	Leu	Glu	Gln	His	Asp	Ser	Cys	Pro	Val	Cys	Arg	Lys	Ser	Leu	
				215					220					225	
Thr	Gly	Gln	Asn	Thr	Ala	Thr	Asn	Pro	Pro	Gly	Leu	Thr	Gly	Val	
				230					235					240	
Ser	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Pro	Ser	
				245					250					255	
Asn	Glu	Asn	Ala	Thr	Ser	Asn	Ser								
				260											

<210> 43

<211> 581

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1798701CD1

<400> 43

Met	Asp	Glu	Asp	Tyr	Tyr	Gly	Ser	Ala	Ala	Glu	Trp	Gly	Asp	Glu	1	5	10	15
Ala	Asp	Gly	Gly	Gln	Gln	Glu	Asp	Asp	Ser	Gly	Glu	Gly	Glu	Asp	20	25	30	35
Asp	Ala	Glu	Val	Gln	Gln	Glu	Cys	Leu	His	Lys	Phe	Ser	Thr	Arg	40	45	50	55
Asp	Tyr	Ile	Met	Glu	Pro	Ser	Ile	Phe	Asn	Thr	Leu	Lys	Arg	Tyr	60	65	70	75
Phe	Gln	Ala	Gly	Gly	Ser	Pro	Glu	Asn	Val	Ile	Gln	Leu	Leu	Ser	80	85	90	95
Glu	Asn	Tyr	Thr	Ala	Val	Ala	Gln	Thr	Val	Asn	Leu	Leu	Ala	Glu	100	105	110	115
Trp	Leu	Ile	Gln	Thr	Gly	Val	Glu	Pro	Val	Gln	Val	Gln	Glu	Thr	120	125	130	135
Val	Glu	Asn	Tyr	Leu	Lys	Ser	Leu	Leu	Ile	Lys	His	Phe	Asp	Pro	140	145	150	155
Arg	Lys	Ala	Asp	Ser	Ile	Phe	Thr	Glu	Glu	Gly	Glu	Thr	Pro	Ala	160	165	170	175
Trp	Leu	Glu	Gln	Met	Ile	Ala	His	Thr	Thr	Trp	Arg	Asp	Leu	Phe	180	185	190	195
Tyr	Lys	Leu	Ala	Glu	Ala	His	Pro	Asp	Cys	Leu	Met	Leu	Asn	Phe	200	205	210	215
Thr	Val	Lys	Leu	Ile	Ser	Asp	Ala	Gly	Tyr	Gln	Gly	Glu	Ile	Thr	220	225	230	235
Ser	Val	Ser	Thr	Ala	Cys	Gln	Gln	Leu	Glu	Val	Phe	Ser	Arg	Val	240	245	250	255
Leu	Arg	Thr	Ser	Leu	Ala	Thr	Ile	Leu	Asp	Gly	Gly	Glu	Glu	Asn	260	265	270	275
Leu	Glu	Lys	Asn	Leu	Pro	Glu	Phe	Ala	Lys	Met	Val	Cys	His	Gly	280	285	290	295
Glu	His	Thr	Tyr	Leu	Phe	Ala	Gln	Ala	Met	Met	Ser	Val	Leu	Ala	300	305	310	315
Gln	Glu	Glu	Gln	Gly	Gly	Ser	Ala	Val	Arg	Arg	Ile	Ala	Gln	Glu	320	325	330	335
Val	Gln	Arg	Phe	Ala	Gln	Glu	Lys	Gly	His	Asp	Ala	Ser	Gln	Ile	340	345	350	355
Thr	Leu	Ala	Leu	Gly	Thr	Ala	Ala	Ser	Tyr	Pro	Arg	Ala	Cys	Gln	360	365	370	375
Ala	Leu	Gly	Ala	Met	Leu	Ser	Lys	Gly	Ala	Leu	Asn	Pro	Ala	Asp	380	385	390	395
Ile	Thr	Val	Leu	Phe	Lys	Met	Phe	Thr	Ser	Met	Asp	Pro	Pro	Pro	400	405	410	415
Val	Glu	Leu	Ile	Arg	Val	Pro	Ala	Phe	Leu	Asp	Leu	Phe	Met	Gln	420	425	430	435
Ser	Leu	Phe	Lys	Pro	Gly	Ala	Arg	Ile	Asn	Gln	Asp	His	Lys	His				
Lys	Tyr	Ile	His	Ile	Leu	Ala	Tyr	Ala	Ala	Ser	Val	Val	Glu	Thr				
Trp	Lys	Lys	Asn	Lys	Arg	Val	Ser	Ile	Asn	Lys	Asp	Glu	Leu	Lys				
Ser	Thr	Ser	Lys	Ala	Val	Glu	Thr	Val	His	Asn	Leu	Cys	Cys	Asn				
Glu	Asn	Lys	Gly	Ala	Ser	Glu	Leu	Val	Ala	Glu	Leu	Ser	Thr	Leu				
Tyr	Gln	Cys	Ile	Arg	Phe	Pro	Val	Val	Ala	Met	Gly	Val	Leu	Lys				
Trp	Val	Asp	Trp	Thr	Val	Ser	Glu	Pro	Arg	Tyr	Phe	Gln	Leu	Gln				


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Thr Asp His Thr Pro Val His Leu Ala Leu Leu Asp Glu Ile Ser
440 445 450
Thr Cys His Gln Leu Leu His Pro Gln Val Leu Gln Leu Leu Val
455 460 465
Lys Leu Phe Glu Thr Glu His Ser Gln Leu Asp Val Met Glu Gln
470 475 480
Leu Glu Leu Lys Lys Thr Leu Leu Asp Arg Met Val His Leu Leu
485 490 495
Ser Arg Gly Tyr Val Leu Pro Val Val Ser Tyr Ile Arg Lys Cys
500 505 510
Leu Glu Lys Leu Asp Thr Asp Ile Ser Leu Ile Arg Tyr Phe Val
515 520 525
Thr Glu Val Leu Asp Val Ile Ala Pro Pro Tyr Thr Ser Asp Phe
530 535 540
Val Gln Leu Phe Leu Pro Ile Leu Glu Asn Asp Ser Ile Ala Gly
545 550 555
Thr Ile Lys Thr Glu Gly Glu His Asp Pro Val Thr Glu Phe Ile
560 565 570
Ala His Cys Lys Ser Asn Phe Ile Met Val Asn
575 580

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<210> 44

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1842496CD1

<400> 44

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Met Gln Lys Ser Cys Glu Glu Asn Glu Gly Lys Pro Gln Asn Met
1 5 10 15
Pro Lys Ala Glu Glu Asp Arg Pro Leu Glu Asp Val Pro Gln Glu
20 25 30
Ala Glu Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln Glu
35 40 45
Ala Glu Gly Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly
50 55 60
Phe Lys Glu Asp Thr Pro Val Arg His Leu Asp Pro Glu Glu Met
65 70 75
Ile Arg Gly Val Asp Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg
80 85 90
Arg Val Arg Asn Lys Phe Val Met Met His Trp Lys Gln Arg His
95 100 105
Ser Arg Ser Arg Pro Tyr Pro Val Cys Phe Arg Pro
110 115

```

<210> 45

<211> 202

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1868613CD1

<400> 45

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Met Ala Lys Val Ser Val Leu Asn Val Ala Val Leu Glu Asn Pro
1 5 10 15
Ser Pro Phe His Ser Pro Phe Arg Phe Glu Ile Ser Phe Glu Cys
20 25 30
Ser Glu Ala Leu Ala Asp Asp Leu Glu Trp Lys Ile Ile Tyr Val

```

	35		40		45
Gly Ser Ala Glu Ser	Glu Glu Phe Asp	Gln Ile Leu Asp Ser	Val		
	50		55		60
Leu Val Gly Pro Val	Pro Ala Gly Arg	His Met Phe Val Phe	Gln		
	65		70		75
Ala Asp Ala Pro Asn	Pro Ser Leu Ile Pro	Glu Thr Asp Ala Val			
	80		85		90
Gly Val Thr Val Val	Leu Ile Thr Cys Thr	Tyr His Gly Gln Glu			
	95		100		105
Phe Ile Arg Val Gly	Tyr Tyr Val Asn Asn	Glu Tyr Leu Asn Pro			
	110		115		120
Glu Leu Arg Glu Asn	Pro Pro Met Lys Pro	Asp Phe Ser Gln Leu			
	125		130		135
Gln Arg Asn Ile Leu	Ala Ser Asn Pro Arg	Val Thr Arg Phe His			
	140		145		150
Ile Asn Trp Asp Asn	Asn Met Asp Arg Leu	Glu Ala Ile Glu Thr			
	155		160		165
Gln Asp Pro Ser Leu	Gly Cys Gly Leu Pro	Leu Asn Cys Thr Pro			
	170		175		180
Ile Lys Gly Leu Gly	Leu Pro Gly Cys Ile	Pro Gly Leu Leu Pro			
	185		190		195
Glu Asn Ser Met Asp	Cys Ile				
	200				

<210> 46

<211> 442

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1870609CD1

<400> 46

Met Leu Val Ala Lys	Leu Ile Gln Cys Ile	Val Phe Gly Pro Leu			
1	5	10		15	
Arg Val Ser Glu Arg	Gln Ser Leu Leu Val	Thr Val Arg Thr Ala			
	20	25		30	
His Val Ile Leu Arg	Tyr Val Ile His Leu	Trp Asp Leu Asn His			
	35	40		45	
Glu Gly Thr Trp Glu	Gly Lys Gly Thr Tyr	Val Tyr Tyr Thr Asp			
	50	55		60	
Phe Val Met Glu Leu	Thr Leu Leu Ser Leu	Asp Leu Met His His			
	65	70		75	
Ile His Met Leu Leu	Phe Gly Asn Ile Trp	Leu Ser Met Ala Ser			
	80	85		90	
Leu Val Ile Phe Met	Gln Leu Arg Tyr Leu	Phe His Glu Val Gln			
	95	100		105	
Arg Arg Ile Arg Arg	His Lys Asn Tyr Leu	Arg Val Val Gly Asn			
	110	115		120	
Met Glu Ala Arg Phe	Ala Val Ala Thr Pro	Glu Glu Leu Ala Val			
	125	130		135	
Asn Asn Asp Asp Cys	Ala Ile Cys Trp Asp	Ser Met Gln Ala Ala			
	140	145		150	
Arg Lys Leu Pro Cys	Gly His Leu Phe His	Asn Ser Cys Leu Arg			
	155	160		165	
Ser Trp Leu Glu Gln	Asp Thr Ser Cys Pro	Thr Cys Arg Met Ser			
	170	175		180	
Leu Asn Ile Ala Asp	Asn Asn Arg Val Arg	Glu Glu His Gln Gly			
	185	190		195	
Glu Asn Leu Asp Glu	Asn Leu Val Pro Val	Ala Ala Ala Glu Gly			
	200	205		210	
Arg Pro Arg Leu Asn	Gln His Asn His Phe	Phe His Phe Asp Gly			

	215		220		225
Ser Arg Ile Ala	Ser Trp Leu Pro Ser	Phe Ser Val Glu Val	Met		
	230		235		240
His Thr Thr Asn	Ile Leu Gly Ile Thr	Gln Ala Ser Asn Ser	Gln		
	245		250		255
Leu Asn Ala Met	Ala His Gln Ile Gln	Glu Met Phe Pro Gln	Val		
	260		265		270
Pro Tyr His Leu	Val Leu Gln Asp Leu	Gln Leu Thr Arg Ser	Val		
	275		280		285
Glu Ile Thr Thr	Asp Asn Ile Leu Glu	Gly Arg Ile Gln Val	Pro		
	290		295		300
Phe Pro Thr Gln	Arg Ser Asp Ser Ile	Arg Pro Ala Leu Asn	Ser		
	305		310		315
Pro Val Glu Arg	Pro Ser Ser Asp Gln	Glu Glu Gly Glu Thr	Ser		
	320		325		330
Ala Gln Thr Glu	Arg Val Pro Leu Asp	Leu Ser Pro Arg Leu	Glu		
	335		340		345
Glu Thr Leu Asp	Phe Gly Glu Val Glu	Val Glu Pro Ser Glu	Val		
	350		355		360
Glu Asp Phe Glu	Ala Arg Gly Ser Arg	Phe Ser Lys Ser Ala	Asp		
	365		370		375
Glu Arg Gln Arg	Met Leu Val Gln Arg	Lys Asp Glu Leu Leu	Gln		
	380		385		390
Gln Ala Arg Lys	Arg Phe Leu Asn Lys	Ser Ser Glu Asp Asp	Ala		
	395		400		405
Ala Ser Glu Ser	Phe Leu Pro Ser Glu	Gly Ala Ser Ser Asp	Pro		
	410		415		420
Val Thr Leu Arg	Arg Arg Met Leu Ala	Ala Ala Ala Glu Arg	Arg		
	425		430		435
Leu Gln Lys Gln	Gln Thr Ser				
	440				

<210> 47

<211> 765

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1871961CD1

<400> 47

Met Phe Ser Gln	Gln Gln Gln Gln	Leu Gln Gln Gln	Gln Gln	
1	5	10	15	
Gln Leu Gln Gln	Leu Gln Gln Gln	Gln Leu Gln Gln	Gln Leu	
	20	25	30	
Gln Gln Gln Gln	Leu Leu Gln Leu	Gln Leu Leu Gln	Gln Ser	
	35	40	45	
Pro Pro Gln Ala	Pro Leu Pro Met	Ala Val Ser Arg	Gly Leu Pro	
	50	55	60	
Pro Gln Gln Pro	Gln Gln Pro Leu	Leu Asn Leu Gln	Gly Thr Asn	
	65	70	75	
Ser Ala Ser Leu	Leu Asn Gly Ser	Met Leu Gln Arg	Ala Leu Leu	
	80	85	90	
Leu Gln Gln Leu	Gln Gly Leu Asp	Gln Phe Ala Met	Pro Pro Ala	
	95	100	105	
Thr Tyr Asp Thr	Ala Gly Leu Thr	Met Pro Thr Ala	Thr Leu Gly	
	110	115	120	
Asn Leu Arg Gly	Tyr Gly Met Ala	Ser Pro Gly Leu	Ala Ala-Pro	
	125	130	135	
Ser Leu Thr Pro	Pro Gln Leu Ala	Thr Pro Asn Leu	Gln Gln Phe	
	140	145	150	
Phe Pro Gln Ala	Thr Arg Gln Ser	Leu Leu Gly	Pro Pro Pro	Val

	155		160		165
Gly Val Pro Met	Asn Pro Ser Gln Phe	Asn Leu Ser Gly Arg	Asn		
	170		175		180
Pro Gln Lys Gln	Ala Arg Thr Ser Ser	Ser Thr Thr Pro Asn	Arg		
	185		190		195
Lys Asp Ser Ser	Ser Gln Thr Met Pro	Val Glu Asp Lys Ser	Asp		
	200		205		210
Pro Pro Glu Gly	Ser Glu Glu Ala Ala	Glu Pro Arg Met Asp	Thr		
	215		220		225
Pro Glu Asp Gln	Asp Leu Pro Pro Cys	Pro Glu Asp Ile Ala	Lys		
	230		235		240
Glu Lys Arg Thr	Pro Ala Pro Glu Pro	Glu Pro Cys Glu Ala	Ser		
	245		250		255
Glu Leu Pro Ala	Lys Arg Leu Arg Ser	Ser Glu Glu Pro Thr	Glu		
	260		265		270
Lys Glu Pro Pro	Gly Gln Leu Gln Val	Lys Ala Gln Pro Gln	Ala		
	275		280		285
Arg Met Thr Val	Pro Lys Gln Thr Gln	Thr Pro Asp Leu Leu	Pro		
	290		295		300
Glu Ala Leu Glu	Ala Gln Val Leu Pro	Arg Phe Gln Pro Arg	Val		
	305		310		315
Leu Gln Val Gln	Ala Gln Val Gln Ser	Gln Thr Gln Pro Arg	Ile		
	320		325		330
Pro Ser Thr Asp	Thr Gln Val Gln Pro	Lys Leu Gln Lys Gln	Ala		
	335		340		345
Gln Thr Gln Thr	Ser Pro Glu His Leu	Val Leu Gln Gln Lys	Gln		
	350		355		360
Val Gln Pro Gln	Leu Gln Gln Glu Ala	Glu Pro Gln Lys Gln	Val		
	365		370		375
Gln Pro Gln Val	Gln Pro Gln Ala His	Ser Gln Gly Pro Arg	Gln		
	380		385		390
Val Gln Leu Gln	Gln Glu Ala Glu Pro	Leu Lys Gln Val Gln	Pro		
	395		400		405
Gln Val Gln Pro	Gln Ala His Ser Gln	Pro Pro Arg Gln Val	Gln		
	410		415		420
Leu Gln Leu Gln	Lys Gln Val Gln Thr	Gln Thr Tyr Pro Gln	Val		
	425		430		435
His Thr Gln Ala	Gln Pro Ser Val Gln	Pro Gln Glu His Pro	Pro		
	440		445		450
Ala Gln Val Ser	Val Gln Pro Pro Glu	Gln Thr His Glu Gln	Pro		
	455		460		465
His Thr Gln Pro	Gln Val Ser Leu Leu	Ala Pro Glu Gln Thr	Pro		
	470		475		480
Val Val Val His	Val Cys Gly Leu Glu	Met Pro Pro Asp Ala	Val		
	485		490		495
Glu Ala Gly Gly	Gly Met Glu Lys Thr	Leu Pro Glu Pro Val	Gly		
	500		505		510
Thr Gln Val Ser	Met Glu Glu Ile Gln	Asn Glu Ser Ala Cys	Gly		
	515		520		525
Leu Asp Val Gly	Glu Cys Glu Asn Arg	Ala Arg Glu Met Pro	Gly		
	530		535		540
Val Trp Gly Ala	Gly Gly Ser Leu Lys	Val Thr Ile Leu Gln	Ser		
	545		550		555
Ser Asp Ser Arg	Ala Phe Ser Thr Val	Pro Leu Thr Pro Val	Pro		
	560		565		570
Arg Pro Ser Asp	Ser Val Ser Ser Thr	Pro Ala Ala Thr Ser	Thr		
	575		580		585
Pro Ser Lys Gln	Ala Leu Gln Phe Phe	Cys Tyr Ile Cys Lys	Ala		
	590		595		600
Ser Cys Ser Ser	Gln Glu Phe Gln Asp	His Met Ser Glu Pro			
	605		610		615
Gln His Gln Gln	Arg Leu Gly Glu Ile	Gln His Met Ser Gln	Ala		
	620		625		630

Cys	Leu	Leu	Ser	Leu	Leu	Pro	Val	Pro	Arg	Asp	Val	Leu	Glu	Thr	
				635						640				645	
Glu	Asp	Glu	Glu	Pro	Pro	Pro	Arg	Arg	Trp	Cys	Asn	Thr	Cys	Gln	
				650						655				660	
Leu	Tyr	Tyr	Met	Gly	Asp	Leu	Ile	Gln	His	Arg	Arg	Thr	Gln	Asp	
				665						670				675	
His	Lys	Ile	Ala	Lys	Gln	Ser	Leu	Arg	Pro	Phe	Cys	Thr	Val	Cys	
				680						685				690	
Asn	Arg	Tyr	Phe	Lys	Thr	Pro	Arg	Lys	Phe	Val	Glu	His	Val	Lys	
				695						700				705	
Ser	Gln	Gly	His	Lys	Asp	Lys	Ala	Lys	Glu	Leu	Lys	Ser	Leu	Glu	
				710						715				720	
Lys	Glu	Ile	Ala	Gly	Gln	Asp	Glu	Asp	His	Phe	Ile	Thr	Val	Asp	
				725						730				735	
Ala	Val	Gly	Cys	Phe	Glu	Gly	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Asp	
				740						745				750	
Glu	Asp	Glu	Glu	Glu	Ile	Glu	Val	Glu	Glu	Glu	Leu	Cys	Ser	Arg	
				755						760				765	

<210> 48

<211> 352

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1876258CD1

<400> 48

Met	Pro	Arg	Ser	Phe	Leu	Val	Lys	Ser	Arg	Lys	Ala	His	Thr	Tyr	
1				5					10					15	
His	Gln	Pro	Arg	Val	Gln	Glu	Asp	Glu	Pro	Leu	Trp	Pro	Pro	Ala	
				20					25					30	
Leu	Thr	Pro	Val	Pro	Arg	Asp	Gln	Ala	Pro	Ser	Asn	Ser	Pro	Val	
				35					40					45	
Leu	Ser	Thr	Leu	Phe	Pro	Asn	Gln	Cys	Leu	Asp	Trp	Thr	Asn	Leu	
				50					55					60	
Lys	Arg	Glu	Pro	Glu	Leu	Glu	Gln	Asp	Gln	Asn	Leu	Ala	Arg	Met	
				65					70					75	
Ala	Pro	Ala	Pro	Glu	Gly	Pro	Ile	Val	Leu	Ser	Arg	Pro	Gln	Asp	
				80					85					90	
Gly	Asp	Ser	Pro	Leu	Ser	Asp	Ser	Pro	Pro	Phe	Tyr	Lys	Pro	Ser	
				95					100					105	
Phe	Ser	Trp	Asp	Thr	Leu	Ala	Thr	Thr	Tyr	Gly	His	Ser	Tyr	Arg	
				110					115					120	
Gln	Ala	Pro	Ser	Thr	Met	Gln	Ser	Ala	Phe	Leu	Glu	His	Ser	Val	
				125					130					135	
Ser	Leu	Tyr	Gly	Ser	Pro	Leu	Val	Pro	Ser	Thr	Glu	Pro	Ala	Leu	
				140					145					150	
Asp	Phe	Ser	Leu	Arg	Tyr	Ser	Pro	Gly	Met	Asp	Ala	Tyr	His	Cys	
				155					160					165	
Val	Lys	Cys	Asn	Lys	Val	Phe	Ser	Thr	Pro	His	Gly	Leu	Glu	Val	
				170					175					180	
His	Val	Arg	Arg	Ser	His	Ser	Gly	Thr	Arg	Pro	Phe	Ala	Cys	Asp	
				185					190					195	
Ile	Cys	Gly	Lys	Thr	Phe	Gly	His	Ala	Val	Ser	Leu	Glu	Gln	His	
				200					205					210	
Thr	His	Val	His	Ser	Gln	Gly	Ile	Pro	Ala	Gly	Ser	Ser	Pro	Glu	
				215					220					225	
Pro	Ala	Pro	Asp	Pro	Pro	Gly	Pro	His	Phe	Leu	Arg	Gln	Glu	Arg	
				230					235					240	
Ser	Phe	Glu	Cys	Arg	Met	Cys	Gly	Lys	Thr	Phe	Lys	Arg	Ser	Ser	

Thr	Leu	Ser	Thr	His	Leu	Leu	Ile	His	Ser	Asp	Thr	Arg	Pro	Tyr	245	250	255
															260	265	270
Pro	Cys	Gln	Phe	Cys	Gly	Lys	Arg	Phe	His	Gln	Lys	Ser	Asp	Met	275	280	285
Lys	Lys	His	Thr	Tyr	Ile	His	Thr	Gly	Glu	Lys	Pro	His	Lys	Cys	290	295	300
Gln	Val	Cys	Gly	Lys	Ala	Phe	Ser	Gln	Ser	Ser	Asn	Leu	Ile	Thr	305	310	315
His	Ser	Arg	Lys	His	Thr	Gly	Phe	Lys	Pro	Phe	Ser	Cys	Glu	Leu	320	325	330
Cys	Thr	Lys	Gly	Phe	Gln	Arg	Lys	Val	Asp	Leu	Arg	Arg	His	Arg	335	340	345
Glu	Ser	Gln	His	Asn	Leu	Lys									350		

<210> 49

<211> 1102

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1929822CD1

<400> 49

Met	Phe	Gln	Leu	Pro	Val	Asn	Asn	Leu	Gly	Ser	Leu	Arg	Lys	Ala	1	5	10	15
Arg	Lys	Thr	Val	Lys	Lys	Ile	Leu	Ser	Asp	Ile	Gly	Leu	Glu	Tyr	20	25	30	35
Cys	Lys	Glu	His	Ile	Glu	Asp	Phe	Lys	Gln	Phe	Glu	Pro	Asn	Asp	40	45	50	55
Phe	Tyr	Leu	Lys	Asn	Thr	Thr	Trp	Glu	Asp	Val	Gly	Leu	Trp	Asp	60	65	70	75
Pro	Ser	Leu	Thr	Lys	Asn	Gln	Asp	Tyr	Arg	Thr	Lys	Pro	Phe	Cys	80	85	90	95
Cys	Ser	Ala	Cys	Pro	Phe	Ser	Ser	Lys	Phe	Phe	Ser	Ala	Tyr	Lys	100	105	110	115
Ser	His	Phe	Arg	Asn	Val	His	Ser	Glu	Asp	Phe	Glu	Asn	Arg	Ile	120	125	130	135
Leu	Leu	Asn	Cys	Pro	Tyr	Cys	Thr	Phe	Asn	Ala	Asp	Lys	Lys	Thr	140	145	150	155
Leu	Glu	Thr	His	Ile	Lys	Ile	Phe	His	Ala	Pro	Asn	Ala	Ser	Ala	160	165	170	175
Pro	Ser	Ser	Ser	Leu	Ser	Thr	Phe	Lys	Asp	Lys	Asn	Lys	Asn	Asp	180	185	190	195
Gly	Leu	Lys	Pro	Lys	Gln	Ala	Asp	Ser	Val	Glu	Gln	Ala	Val	Tyr	200	205	210	215
Tyr	Cys	Lys	Lys	Cys	Thr	Tyr	Arg	Asp	Pro	Leu	Tyr	Glu	Ile	Val	220	225	230	235
Arg	Lys	His	Ile	Tyr	Arg	Glu	His	Phe	Gln	His	Val	Ala	Ala	Pro	240	245	250	255
Tyr	Ile	Ala	Lys	Ala	Gly	Glu	Lys	Ser	Leu	Asn	Gly	Ala	Val	Pro	260	265	270	275
Leu	Gly	Ser	Asn	Ala	Arg	Glu	Glu	Ser	Ser	Ile	His	Cys	Lys	Arg	280	285	290	295
Cys	Leu	Phe	Met	Pro	Lys	Ser	Tyr	Glu	Ala	Leu	Val	Gln	His	Val	300	305	310	315
Ile	Glu	Asp	His	Glu	Arg	Ile	Gly	Tyr	Gln	Val	Thr	Ala	Met	Ile	320	325	330	335
Gly	His	Thr	Asn	Val	Val	Val	Pro	Arg	Ser	Lys	Pro	Leu	Met	Leu	340	345	350	355
Ile	Ala	Pro	Lys	Pro	Gln	Asp	Lys	Lys	Ser	Met	Gly	Leu	Pro	Pro	360	365	370	375

	275		280		285
Arg Ile Gly Ser	Leu Ala Ser Gly Asn	Val Arg Ser Leu Pro	Ser		
	290		295		300
Gln Gln Met Val	Asn Arg Leu Ser Ile	Pro Lys Pro Asn Leu	Asn		
	305		310		315
Ser Thr Gly Val	Asn Met Met Ser Ser	Val His Leu Gln Gln	Asn		
	320		325		330
Asn Tyr Gly Val	Lys Ser Val Gly Gln	Gly Tyr Ser Val Gly	Gln		
	335		340		345
Ser Met Arg Leu	Gly Leu Gly Gly Asn	Ala Pro Val Ser Ile	Pro		
	350		355		360
Gln Gln Ser Gln	Ser Val Lys Gln Leu	Leu Pro Ser Gly Asn	Gly		
	365		370		375
Arg Ser Tyr Gly	Leu Gly Ser Glu Gln	Arg Ser Gln Ala Pro	Ala		
	380		385		390
Arg Tyr Ser Leu	Gln Ser Ala Asn Ala	Ser Ser Leu Ser Ser	Gly		
	395		400		405
Gln Leu Lys Ser	Pro Ser Leu Ser Gln	Ser Gln Ala Ser Arg	Val		
	410		415		420
Leu Gly Gln Ser	Ser Ser Lys Pro Ala	Ala Ala Ala Thr Gly	Pro		
	425		430		435
Pro Pro Gly Asn	Thr Ser Ser Thr Gln	Lys Trp Lys Ile Cys	Thr		
	440		445		450
Ile Cys Asn Glu	Leu Phe Pro Glu Asn	Val Tyr Ser Val His	Phe		
	455		460		465
Glu Lys Glu His	Lys Ala Glu Lys Val	Pro Ala Val Ala Asn	Tyr		
	470		475		480
Ile Met Lys Ile	His Asn Phe Thr Ser	Lys Cys Leu Tyr Cys	Asn		
	485		490		495
Arg Tyr Leu Pro	Thr Asp Thr Leu Leu	Asn His Met Leu Ile	His		
	500		505		510
Gly Leu Ser Cys	Pro Tyr Cys Arg Ser	Thr Phe Asn Asp Val	Glu		
	515		520		525
Lys Met Ala Ala	His Met Arg Met Val	His Ile Asp Glu Glu	Met		
	530		535		540
Gly Pro Lys Thr	Asp Ser Thr Leu Ser	Phe Asp Leu Thr Leu	Gln		
	545		550		555
Gln Gly Ser His	Thr Asn Ile His Leu	Leu Val Thr Thr Tyr	Asn		
	560		565		570
Leu Arg Asp Ala	Pro Ala Glu Ser Val	Ala Tyr His Ala Gln	Asn		
	575		580		585
Asn Pro Pro Val	Pro Pro Lys Pro Gln	Pro Lys Val Gln Glu	Lys		
	590		595		600
Ala Asp Ile Pro	Val Lys Ser Ser Pro	Gln Ala Ala Val Pro	Tyr		
	605		610		615
Lys Lys Asp Val	Gly Lys Thr Leu Cys	Pro Leu Cys Phe Ser	Ile		
	620		625		630
Leu Lys Gly Pro	Ile Ser Asp Ala Leu	Ala His His Leu Arg	Glu		
	635		640		645
Arg His Gln Val	Ile Gln Thr Val His	Pro Val Glu Lys Lys	Leu		
	650		655		660
Thr Tyr Lys Cys	Ile His Cys Leu Gly	Val Tyr Thr Ser Asn	Met		
	665		670		675
Thr Ala Ser Thr	Ile Thr Leu His Leu	Val His Cys Arg Gly	Val		
	680		685		690
Gly Lys Thr Gln	Asn Gly Gln Asp Lys	Thr Asn Ala Pro Ser	Arg		
	695		700		705
Leu Asn Gln Ser	Pro Ser Leu Ala Pro	Val Lys Arg Thr Tyr	Glu		
	710		715		720
Gln Met Glu Phe	Pro Leu Leu Lys Lys	Arg Lys Leu Asp Asp	Asp		
	725		730		735
Ser Asp Ser Pro	Ser Phe Phe Glu Glu	Lys Pro Glu Glu Pro	Val		
	740		745		750

Val Leu Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu
 755 760
 Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr
 770 775 780
 Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu
 785 790 795
 Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys Arg Lys Lys
 800 805 810
 Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu Leu Gly
 815 820 825
 Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp Phe
 830 835 840
 Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg
 845 850 855
 Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu Gly Lys
 860 865 870
 Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu Glu
 875 880 885
 Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu
 890 895 900
 Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val
 905 910 915
 Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys
 920 925 930
 Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro
 935 940 945
 Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
 950 955 960
 Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly
 965 970 975
 Pro Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu
 980 985 990
 Met Lys Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp
 995 1000 1005
 Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln
 1010 1015 1020
 Gly Asp Arg Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys
 1025 1030 1035
 Val Glu Gly Phe Trp Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala
 1040 1045 1050
 Ser Glu Asn Asp Glu Arg Leu Ser Asn Pro Gln Ile Glu Trp Gln
 1055 1060 1065
 Asn Ser Thr Ile Asp Ser Glu Asp Gly Glu Gln Phe Asp Asn Met
 1070 1075 1080
 Thr Asp Gly Val Ala Glu Pro Met His Gly Ser Leu Ala Gly Val
 1085 1090 1095
 Lys Leu Ser Ser Gln Gln Ala
 1100

<210> 50

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1970095CD1

<400> 50

Met Gly Arg Ile Phe Leu Asp His Ile Gly Gly Thr Arg Leu Phe
 1 5 10 15
 Ser Cys Ala Asn Cys Asp Thr Ile Leu Thr Asn Arg Ser Glu Leu
 20 25 30


```

Ile Ser Thr Arg Phe Thr Gly Ala Thr Gly Arg Ala Phe Leu Phe
      35      40      45
Asn Lys Val Val Asn Leu Gln Tyr Ser Glu Val Gln Asp Arg Val
      50      55      60
Met Leu Thr Gly Arg His Met Val Arg Asp Val Ser Cys Lys Asn
      65      70      75
Cys Asn Ser Lys Leu Gly Trp Ile Tyr Glu Phe Ala Thr Glu Asp
      80      85      90
Ser Gln Arg Tyr Lys Glu Gly Arg Val Ile Leu Glu Arg Ala Leu
      95     100     105
Val Arg Glu Ser Glu Gly Phe Glu Glu His Val Pro Ser Asp Asn
      110     115     120
Ser

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<210> 51
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1975473CD1

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<400> 51
Met Pro Gly Pro Gly Thr Leu Ser Val Arg Val Ser Pro Pro Gln
  1      5      10      15
Pro Ile Leu Ser Arg Gly Arg Pro Asp Ser Asn Lys Thr Glu Asn
      20      25      30
Arg Arg Ile Thr His Ile Ser Ala Glu Gln Lys Arg Arg Phe Asn
      35      40      45
Ile Lys Leu Gly Phe Asp Thr Leu His Gly Leu Val Ser Thr Leu
      50      55      60
Ser Ala Gln Pro Ser Leu Lys Val Ser Lys Ala Thr Thr Leu Gln
      65      70      75
Lys Thr Ala Glu Tyr Ile Leu Met Leu Gln Gln Glu Arg Ala Gly
      80      85      90
Leu Gln Glu Glu Ala Gln Gln Leu Arg Asp Glu Ile Glu Glu Leu
      95     100     105
Asn Ala Ala Ile Asn Leu Cys Gln Gln Gln Leu Pro Ala Thr Gly
      110     115     120
Val Pro Ile Thr His Gln Arg Phe Asp Gln Met Arg Asp Met Phe
      125     130     135
Asp Asp Tyr Val Arg Thr Arg Thr Leu His Asn Trp Lys Phe Trp
      140     145     150
Val Phe Ser Ile Leu Ile Arg Pro Leu Phe Glu Ser Phe Asn Gly
      155     160     165
Met Val Ser Thr Ala Ser Val His Thr Leu Arg Gln Thr Ser Leu
      170     175     180
Ala Trp Leu Asp Gln Tyr Cys Ser Leu Pro Ala Leu Arg Pro Thr
      185     190     195
Val Leu Asn Ser Leu Arg Gln Leu Gly Thr Ser Thr Ser Ile Leu
      200     205     210
Thr Asp Pro Gly Arg Ile Pro Glu Gln Ala Thr Arg Ala Val Thr
      215     220     225
Glu Gly Thr Leu Gly Lys Pro Leu
      230

```

<210> 52
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1976527CD1

<400> 52

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Met Ala Glu Arg Pro Glu Asp Leu Asn Leu Pro Asn Ala Val Ile
 1          5          10          15
Thr Arg Ile Ile Lys Glu Ala Leu Pro Asp Gly Val Asn Ile Ser
          20          25          30
Lys Glu Ala Arg Ser Ala Ile Ser Arg Ala Ala Ser Val Phe Val
          35          40          45
Leu Tyr Ala Thr Ser Cys Ala Asn Asn Phe Ala Met Lys Gly Lys
          50          55          60
Arg Lys Thr Leu Asn Ala Ser Asp Val Leu Ser Ala Met Glu Glu
          65          70          75
Met Glu Phe Gln Arg Phe Val Thr Pro Leu Lys Glu Ala Leu Glu
          80          85          90
Ala Tyr Arg Arg Glu Gln Lys Gly Lys Glu Ala Ser Glu Gln
          95          100          105
Lys Lys Lys Asp Lys Asp Lys Lys Thr Asp Ser Glu Glu Gln Asp
          110          115          120
Lys Ser Arg Asp Glu Asp Asn Asp Glu Asp Glu Glu Arg Leu Glu
          125          130          135
Glu Glu Glu Gln Asn Glu Glu Glu Glu Val Asp Asn
          140          145

```

<210> 53

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2108023CD1

<400> 53

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Met Ala Glu Val Glu Glu Thr Leu Lys Arg Ile Gln Ser His Lys
 1          5          10          15
Gly Val Ile Gly Thr Met Val Val Asn Ala Glu Gly Ile Pro Ile
          20          25          30
Arg Thr Thr Leu Asp Asn Ser Thr Thr Val Gln Tyr Ala Gly Leu
          35          40          45
Leu His His Leu Thr Met Lys Ala Lys Ser Thr Val Arg Asp Ile
          50          55          60
Asp Pro Gln Asn Asp Leu Thr Phe Leu Arg Ile Arg Ser Lys Lys
          65          70          75
His Glu Ile Met Val Ala Pro Asp Lys Glu Tyr Leu Leu Ile Val
          80          85          90
Ile Gln Asn Pro Cys Glu
          95

```

<210> 54

<211> 259

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2135746CD1

<400> 54

```

Met Arg Asp Arg Arg Gly Pro Leu Gly Thr Cys Leu Ala Gln Val
 1          5          10          15

```

Gln Gln Ala Gly Gly Gly Asp Ser Asp Lys Leu Ser Cys Ser Leu
 20 25 30
 Lys Lys Arg Met Pro Glu Gly Pro Trp Pro Ala Asp Ala Pro Ser
 35 40 45
 Trp Met Asn Lys Pro Val Val Asp Gly Asn Ser Gln Ser Glu Ala
 50 55 60
 Leu Ser Leu Glu Met Arg Lys Asp Pro Ser Gly Ala Gly Leu Trp
 65 70 75
 Leu His Ser Gly Gly Pro Val Leu Pro Tyr Val Arg Glu Ser Val
 80 85 90
 Arg Arg Asn Pro Ala Ser Ala Ala Thr Pro Ser Thr Ala Val Gly
 95 100 105
 Leu Phe Pro Ala Pro Thr Glu Cys Phe Ala Arg Val Ser Cys Ser
 110 115 120
 Gly Val Glu Ala Leu Gly Arg Arg Asp Trp Leu Gly Gly Gly Pro
 125 130 135
 Arg Ala Thr Asp Gly His Arg Gly Gln Cys Pro Lys Gly Glu Pro
 140 145 150
 Arg Val Ser Arg Leu Pro Arg His Gln Lys Leu Pro Glu Met Gly
 155 160 165
 Ser Phe Gln Asp Asp Pro Pro Ser Ala Phe Pro Lys Gly Leu Gly
 170 175 180
 Ser Glu Leu Glu Pro Ala Cys Leu His Ser Ile Leu Ser Ala Thr
 185 190 195
 Leu His Met Tyr Pro Glu Val Leu Leu Ser Glu Glu Thr Lys Arg
 200 205 210
 Ile Phe Leu Asp Arg Leu Lys Pro Met Phe Ser Lys Gln Thr Ile
 215 220 225
 Glu Phe Lys Lys Met Leu Lys Ser Thr Ser Asp Gly Leu Gln Ile
 230 235 240
 Thr Leu Gly Leu Leu Ala Leu Gln Pro Phe Glu Leu Ala Asn Thr
 245 250 255
 Leu Cys His Ser

<210> 55

<211> 474

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2154810CD1

<400> 55

Met Ala Leu Arg Ser Val Met Phe Ser Asp Val Ser Ile Asp Phe
 1 5 10 15
 Ser Pro Glu Gly Trp Glu Tyr Leu Asp Leu Glu Gln Lys Asp Leu
 20 25 30
 Tyr Arg Asp Val Met Leu Glu Asn Tyr Ser Asn Leu Val Ser Leu
 35 40 45
 Gly Cys Phe Ile Ser Lys Pro Asp Val Ile Ser Ser Leu Glu Gln
 50 55 60
 Gly Lys Glu Pro Trp Lys Val Val Arg Lys Gly Arg Arg Gln Tyr
 65 70 75
 Pro Asp Leu Glu Thr Lys Tyr Glu Thr Lys Lys Leu Ser Leu Glu
 80 85 90
 Asn Asp Ile Tyr Glu Ile Asn Leu Ser Gln Trp Lys Ile Met Glu
 95 100 105
 Arg Ile Glu Asn His Gly Leu Lys Gly Leu Ile Leu Lys Asn Asp
 110 115 120
 Trp Glu Ser Thr Gly Lys Ile Glu Gly Gln Glu Arg Pro Gln Glu
 125 130 135

Gly	Tyr	Phe	Ser	Ser	Val	Lys	Met	Pro	Ser	Glu	Lys	Val	Ser	Ser	
				140					145					150	
Tyr	Gln	Lys	Arg	Thr	Ser	Val	Thr	Pro	His	Gln	Arg	Leu	His	Phe	
				155					160					165	
Val	Asp	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Arg	
				170					175					180	
Val	Arg	Gln	Gln	Leu	Thr	Phe	His	His	Arg	Ile	His	Thr	Gly	Glu	
				185					190					195	
Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Met	Ala	Phe	Arg	Gln	Thr	
				200					205					210	
Ala	His	Leu	Thr	Arg	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	
				215					220					225	
Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Arg	Gly	Tyr	His	
				230					235					240	
Leu	Ser	Gln	His	Gln	Lys	Ile	His	Thr	Gly	Glu	Lys	Pro	Phe	Glu	
				245					250					255	
Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Trp	Gly	Ser	Ser	Leu	Val	
				260					265					270	
Lys	His	Glu	Arg	Val	His	Thr	Gly	Glu	Lys	Ser	His	Glu	Cys	Lys	
				275					280					285	
Glu	Cys	Gly	Lys	Thr	Phe	Cys	Ser	Gly	Tyr	Gln	Leu	Thr	Arg	His	
				290					295					300	
Gln	Val	Phe	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	
				305					310					315	
Gly	Lys	Ala	Phe	Asn	Cys	Gly	Ser	Ser	Leu	Val	Gln	His	Glu	Arg	
				320					325					330	
Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	
				335					340					345	
Ala	Phe	Ser	Arg	Gly	Tyr	His	Leu	Thr	Gln	His	Gln	Lys	Ile	His	
				350					355					360	
Thr	Gly	Glu	Lys	Pro	Phe	Lys	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	
				365					370					375	
Ser	Trp	Gly	Ser	Ser	Leu	Val	Lys	His	Glu	Arg	Val	His	Thr	Asn	
				380					385					390	
Glu	Lys	Ser	Tyr	Glu	Cys	Lys	Asp	Cys	Gly	Lys	Ala	Phe	Gly	Ser	
				395					400					405	
Gly	Tyr	Gln	Leu	Ser	Val	His	Gln	Arg	Phe	His	Thr	Gly	Glu	Lys	
				410					415					420	
Leu	Tyr	Gln	His	Lys	Glu	Phe	Gly	Lys	Thr	Phe	Thr	Arg	Gly	Ser	
				425					430					435	
Lys	Leu	Val	His	Glu	Arg	Thr	His	Ser	Asn	Asp	Lys	Pro	Tyr	Glu	
				440					445					450	
Cys	Asn	Glu	Cys	Gly	Glu	Ala	Phe	Leu	Trp	Thr	Thr	Tyr	Ser	Asn	
				455					460					465	
Glu	Lys	Ile	Asp	Thr	Asp	Glu	Thr	Leu							
				470											

<210> 56

<211> 231

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2228991CD1

<400> 56

Met	Ser	His	Gly	Asn	Lys	Glu	Val	Phe	Ser	Cys	Arg	Gly	Ile	Leu	
1				5					10					15	
Leu	Ala	Val	Asn	Trp	Phe	Leu	Glu	Arg	Gly	His	Thr	Asp	Ile	Thr	
				20					25					30	
Val	Phe	Val	Pro	Ser	Trp	Arg	Lys	Glu	Gln	Pro	Arg	Pro	Asp	Val	
				35					40					45	

```

Pro Ile Thr Asp Gln His Ile Leu Arg Glu Leu Glu Lys Lys Lys
    50          55          60
Ile Leu Val Phe Thr Pro Ser Arg Arg Val Gly Gly Lys Arg Val
    65          70          75
Val Cys Tyr Asp Asp Arg Phe Ile Val Lys Leu Ala Tyr Glu Ser
    80          85          90
Asp Gly Ile Val Val Ser Asn Asp Thr Tyr Arg Asp Leu Gln Gly
    95          100         105
Glu Arg Gln Glu Trp Lys Arg Phe Ile Glu Glu Arg Leu Leu Met
   110         115         120
Tyr Ser Phe Val Asn Asp Lys Phe Met Pro Pro Asp Asp Pro Leu
   125         130         135
Gly Arg His Gly Pro Ser Leu Asp Asn Phe Leu Arg Lys Lys Pro
   140         145         150
Leu Thr Leu Glu His Arg Lys Gln Pro Cys Pro Tyr Gly Arg Lys
   155         160         165
Cys Thr Tyr Gly Ile Lys Cys Arg Phe Phe His Pro Glu Arg Pro
   170         175         180
Ser Cys Pro Gln Arg Ser Val Ala Asp Glu Leu Arg Ala Asn Ala
   185         190         195
Leu Leu Ser Pro Pro Arg Ala Pro Ser Lys Asp Lys Asn Gly Arg
   200         205         210
Arg Pro Ser Pro Ser Ser Gln Ser Ser Ser Leu Leu Thr Glu Ser
   215         220         225
Glu Gln Cys Ser Leu Asp
    230

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<210> 57

<211> 456

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2241206CD1

<400> 57

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Met Asp Ser Arg Leu Gln Glu Ile Arg Glu Arg Gln Lys Leu Arg
  1      5      10      15
Arg Gln Leu Leu Ala Gln Gln Leu Gly Ala Glu Ser Ala Asp Ser
   20     25     30
Ile Gly Ala Val Leu Asn Ser Lys Asp Glu Gln Arg Glu Ile Ala
   35     40     45
Glu Thr Arg Glu Thr Cys Arg Ala Ser Tyr Asp Thr Ser Ala Pro
   50     55     60
Asn Ala Lys Arg Lys Tyr Leu Asp Glu Gly Glu Thr Asp Glu Asp
   65     70     75
Lys Met Glu Glu Tyr Lys Asp Glu Leu Glu Met Gln Gln Asp Glu
   80     85     90
Glu Asn Leu Pro Tyr Glu Glu Glu Ile Tyr Lys Asp Ser Ser Thr
   95    100    105
Phe Leu Lys Gly Thr Gln Ser Leu Asn Pro His Asn Asp Tyr Cys
  110    115    120
Gln His Phe Val Asp Thr Gly His Arg Pro Gln Asn Phe Ile Arg
  125    130    135
Asp Val Gly Leu Ala Asp Arg Phe Glu Glu Tyr Pro Lys Leu Arg
  140    145    150
Glu Leu Ile Arg Leu Lys Asp Glu Leu Ile Ala Lys Ser Asn Thr
  155    160    165
Pro Pro Met Tyr Leu Gln Ala Asp Ile Glu Ala Phe Asp Ile Arg
  170    175    180
Glu Leu Thr Pro Lys Phe Asp Val Ile Leu Leu Glu Pro Pro Leu
  185    190    195

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Glu Glu Tyr Tyr Arg Glu Thr Gly Ile Thr Ala Asn Glu Lys Cys
 200 205 210
 Trp Thr Trp Asp Asp Ile Met Lys Leu Glu Ile Asp Glu Ile Ala
 215 220 225
 Ala Pro Arg Ser Phe Ile Phe Leu Trp Cys Gly Ser Gly Glu Gly
 230 235 240
 Leu Asp Leu Gly Arg Val Cys Leu Arg Lys Trp Gly Tyr Arg Arg
 245 250 255
 Cys Glu Asp Ile Cys Trp Ile Lys Thr Asn Lys Asn Asn Pro Gly
 260 265 270
 Lys Thr Lys Thr Leu Asp Pro Lys Ala Val Phe Gln Arg Thr Lys
 275 280 285
 Glu His Cys Leu Met Gly Ile Lys Gly Thr Val Lys Arg Ser Thr
 290 295 300
 Asp Gly Asp Phe Ile His Ala Asn Val Asp Ile Asp Leu Ile Ile
 305 310 315
 Thr Glu Glu Pro Glu Ile Gly Asn Ile Glu Lys Pro Val Glu Ile
 320 325 330
 Phe His Ile Ile Glu His Phe Cys Leu Gly Arg Arg Arg Leu His
 335 340 345
 Leu Phe Gly Arg Asp Ser Thr Ile Arg Pro Gly Trp Leu Thr Val
 350 355 360
 Gly Pro Thr Leu Thr Asn Ser Asn Tyr Asn Ala Glu Thr Tyr Ala
 365 370 375
 Ser Tyr Phe Ser Ala Pro Asn Ser Tyr Leu Thr Gly Cys Thr Glu
 380 385 390
 Glu Ile Glu Arg Leu Arg Pro Lys Ser Pro Pro Pro Lys Ser Lys
 395 400 405
 Ser Asp Arg Gly Gly Gly Ala Pro Arg Gly Gly Gly Arg Gly Gly
 410 415 420
 Thr Ser Ala Gly Arg Gly Arg Glu Arg Asn Arg Ser Asn Phe Arg
 425 430 435
 Gly Glu Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly Ala His Arg
 440 445 450
 Gly Gly Phe Pro Pro Arg
 455

<210> 58

<211> 159

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2259590CD1

<400> 58

Met Ser Ala Ala Ile Pro Pro Pro Gln Ala Ser Ala Lys Pro Phe
 1 5 10 15
 Leu Gly Pro Trp Arg Gln Pro Val Ser Ser Arg Arg Ala Glu Ala
 20 25 30
 Ala Pro Arg Thr Leu Cys Ala Phe Tyr Thr Thr Ala Gly Thr Glu
 35 40 45
 Val Pro Arg Ser Pro Glu Pro Glu Pro Gly Val Gly Arg Ala Arg
 50 55 60
 Arg Thr Gly Phe Leu Ala Asp Ser His Gly Leu Thr Gln Pro Pro
 65 70 75
 Gly Pro Met Ala Ala Pro Ala Leu Ala Leu Val Ser Phe Glu Asp
 80 85 90
 Val Val Val Thr Phe Thr Gly Glu Glu Trp Gly His Leu Asp Leu
 95 100 105
 Ala Gln Arg Thr Leu Tyr Gln Glu Val Met Leu Glu Thr Cys Arg
 110 115 120

Leu Leu Val Ser Leu Gly His Pro Val Pro Lys Pro Glu Leu Ile
 125 130 135
 Tyr Leu Leu Glu His Gly Gln Glu Leu Trp Thr Val Lys Arg Gly
 140 145 150
 Leu Ser Gln Ser Thr Cys Ala Gly Trp
 155

<210> 59
 <211> 260
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2307537CD1

<400> 59
 Met Pro Val Asp Phe Cys Thr Thr Arg Val Ser Pro Ala His Arg
 1 5 10 15
 Ser Pro Thr Val Leu Cys Gln Lys Val Cys Glu Glu Asn Ser Val
 20 25 30
 Ser Pro Ile Gly Cys Asn Ser Ser Asp Pro Ala Asp Phe Glu Pro
 35 40 45
 Ile Pro Ser Phe Ser Gly Phe Pro Leu Asp Ser Pro Lys Thr Leu
 50 55 60
 Val Leu Asp Phe Glu Thr Glu Gly Glu Arg Asn Ser Pro Asn Pro
 65 70 75
 Arg Ser Val Arg Ile Pro Ser Pro Asn Ile Leu Lys Thr Gly Leu
 80 85 90
 Thr Glu Asn Val Asp Arg Gly Leu Gly Gly Leu Glu Gly Thr His
 95 100 105
 Gln Ala Leu Asp Leu Leu Ala Gly Gly Met Met Pro Glu Glu Val
 110 115 120
 Lys Glu Ser Ser Gln Leu Asp Lys Gln Glu Ser Leu Gly Leu Glu
 125 130 135
 Leu Lys Thr Ile Asn Ser Ala Gly Leu Gly Pro Ser Pro Cys Leu
 140 145 150
 Pro Asp Leu Val Asp Phe Val Thr Arg Thr Ser Gly Val Gln Lys
 155 160 165
 Asp Lys Leu Cys Ser Pro Leu Ser Glu Pro Gly Asp Pro Ser Lys
 170 175 180
 Cys Ser Ser Leu Glu Leu Gly Pro Leu Gln Leu Glu Ile Ser Asn
 185 190 195
 Ala Ser Thr Thr Glu Val Ala Ile Leu Gln Val Asp Asp Asp Ser
 200 205 210
 Gly Asp Pro Leu Asn Leu Val Lys Ala Pro Val Ser Arg Ser Pro
 215 220 225
 Pro Arg Glu Gln Val Ile Glu Asp Asn Met Val Pro Gln Gly Met
 230 235 240
 Pro Glu Gln Glu Thr Thr Val Gly Ala Ile Gln Asp His Thr Glu
 245 250 255
 Ser Ser Val His Asn
 260

<210> 60
 <211> 352
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2440675CD1

<400> 60

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Met Pro Arg Ser Phe Leu Val Lys Ser Arg Lys Ala His Thr Tyr
 1          5          10          15
His Gln Pro Arg Val Gln Glu Asp Glu Pro Leu Trp Pro Pro Ala
          20          25          30
Leu Thr Pro Val Pro Arg Asp Gln Ala Pro Ser Asn Ser Pro Val
          35          40          45
Leu Ser Thr Leu Phe Pro Asn Gln Cys Leu Asp Trp Thr Asn Leu
          50          55          60
Lys Arg Glu Pro Glu Leu Glu Gln Asp Gln Asn Leu Ala Arg Met
          65          70          75
Ala Pro Ala Pro Glu Gly Pro Ile Val Leu Ser Arg Pro Gln Asp
          80          85          90
Gly Asp Ser Pro Leu Ser Asp Ser Pro Pro Phe Tyr Lys Pro Ser
          95          100          105
Phe Ser Trp Asp Thr Leu Ala Thr Thr Tyr Gly His Ser Tyr Arg
          110          115          120
Gln Ala Pro Ser Thr Met Gln Ser Ala Phe Leu Glu His Ser Val
          125          130          135
Ser Leu Tyr Gly Ser Pro Leu Val Pro Ser Thr Glu Pro Ala Leu
          140          145          150
Asp Phe Ser Leu Arg Tyr Ser Pro Gly Met Asp Ala Tyr His Cys
          155          160          165
Val Lys Cys Asn Lys Val Phe Ser Thr Pro His Gly Leu Glu Val
          170          175          180
His Val Arg Arg Ser His Ser Gly Thr Arg Pro Phe Ala Cys Asp
          185          190          195
Ile Cys Gly Lys Thr Phe Gly His Ala Val Ser Leu Glu Gln His
          200          205          210
Thr His Val His Ser Gln Gly Ile Pro Ala Gly Ser Ser Pro Glu
          215          220          225
Pro Ala Pro Asp Pro Pro Gly Pro His Phe Leu Arg Gln Glu Arg
          230          235          240
Ser Phe Glu Cys Arg Met Cys Gly Lys Thr Phe Lys Arg Ser Ser
          245          250          255
Thr Leu Ser Thr His Leu Leu Ile His Ser Asp Thr Arg Pro Tyr
          260          265          270
Pro Cys Gln Phe Cys Gly Lys Arg Phe His Gln Lys Ser Asp Met
          275          280          285
Lys Lys His Thr Tyr Ile His Thr Gly Glu Lys Pro His Lys Cys
          290          295          300
Gln Val Cys Gly Lys Ala Phe Ser Gln Ser Ser Asn Leu Ile Thr
          305          310          315
His Ser Arg Lys His Thr Gly Phe Lys Pro Phe Ser Cys Glu Leu
          320          325          330
Cys Thr Lys Gly Phe Gln Arg Lys Val Asp Leu Arg Arg His Arg
          335          340          345
Glu Ser Gln His Asn Leu Lys
          350

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<210> 61

<211> 467

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No.: 2463542CD1

<400> 61

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Met Arg Thr Tyr Val Cys His Ile Cys Ser Ile Ala Phe Thr Ser
 1          5          10          15
Leu Asp Met Phe Arg Ser His Met Gln Gly Gly Glu His Gln Ile

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	20		25		30
Lys Glu Ser Ile Val Ile Asn Leu Val Lys Asn Ser Arg Lys Thr					
	35		40		45
Gln Asp Ser Tyr Gln Asn Glu Cys Ala Asp Tyr Ile Asn Val Gln					
	50		55		60
Lys Ala Arg Gly Leu Glu Ala Lys Thr Cys Phe Arg Lys Met Glu					
	65		70		75
Glu Ser Ser Leu Glu Thr Cys Arg Tyr Arg Glu Val Val Asp Ser					
	80		85		90
Arg Pro Arg His Arg Met Phe Glu Gln Arg Leu Pro Phe Glu Thr					
	95		100		105
Phe Arg Thr Tyr Ala Ala Pro Tyr Asn Ile Ser Gln Ala Met Glu					
	110		115		120
Lys Gln Leu Pro His Ser Lys Lys Thr Tyr Asp Ser Phe Gln Asp					
	125		130		135
Glu Leu Glu Asp Tyr Ile Lys Val Gln Lys Ala Arg Gly Leu Asp					
	140		145		150
Pro Lys Thr Cys Phe Arg Lys Met Arg Glu Asn Ser Val Asp Thr					
	155		160		165
His Gly Tyr Arg Glu Met Val Asp Ser Gly Pro Arg Ser Arg Met					
	170		175		180
Cys Glu Gln Arg Phe Ser His Glu Ala Ser Gln Thr Tyr Gln Arg					
	185		190		195
Pro Tyr His Ile Ser Pro Val Glu Ser Gln Leu Pro Gln Trp Leu					
	200		205		210
Pro Thr His Ser Lys Arg Thr Tyr Asp Ser Phe Gln Asp Glu Leu					
	215		220		225
Glu Asp Tyr Ile Lys Val Gln Lys Ala Arg Gly Leu Glu Pro Lys					
	230		235		240
Thr Cys Phe Arg Lys Ile Gly Asp Ser Ser Val Glu Thr His Arg					
	245		250		255
Asn Arg Glu Met Val Asp Val Arg Pro Arg His Arg Met Leu Glu					
	260		265		270
Gln Lys Leu Pro Cys Glu Thr Phe Gln Thr Tyr Ser Gly Pro Tyr					
	275		280		285
Ser Ile Ser Gln Val Val Glu Asn Gln Leu Pro His Cys Leu Pro					
	290		295		300
Ala His Asp Ser Lys Gln Arg Leu Asp Ser Ile Ser Tyr Cys Gln					
	305		310		315
Leu Thr Arg Asp Cys Phe Pro Glu Lys Pro Val Pro Leu Ser Leu					
	320		325		330
Asn Gln Gln Glu Asn Asn Ser Gly Ser Tyr Ser Val Glu Ser Glu					
	335		340		345
Val Tyr Lys His Leu Ser Ser Glu Asn Asn Thr Ala Asp His Gln					
	350		355		360
Ala Gly His Lys Arg Lys His Gln Lys Arg Lys Arg His Leu Glu					
	365		370		375
Glu Gly Lys Glu Arg Pro Glu Lys Glu Gln Ser Lys His Lys Arg					
	380		385		390
Lys Lys Ser Tyr Glu Asp Thr Asp Leu Asp Lys Asp Lys Ser Ile					
	395		400		405
Arg Gln Arg Lys Arg Glu Glu Asp Arg Val Lys Val Ser Ser Gly					
	410		415		420
Lys Leu Lys His Arg Lys Lys Lys Lys Ser His Asp Val Pro Ser					
	425		430		435
Glu Lys Glu Glu Arg Lys His Arg Lys Glu Lys Lys Lys Ser Val					
	440		445		450
Glu Glu Arg Thr Glu Glu Glu Met Leu Trp Asp Glu Ser Ile Leu					
	455		460		465
Gly Phe					

<210> 62

<211> 550
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2486031CD1

<400> 62

Met	Val	Arg	Gly	Trp	Glu	Pro	Pro	Pro	Gly	Leu	Asp	Cys	Ala	Ile	1	5	10	15
Ser	Glu	Gly	His	Lys	Ser	Glu	Gly	Thr	Met	Pro	Pro	Asn	Lys	Glu	20	25	30	35
Ala	Ser	Gly	Leu	Ser	Ser	Ser	Pro	Ala	Gly	Leu	Ile	Cys	Leu	Pro	40	45	50	55
Pro	Ile	Ser	Glu	Glu	Leu	Gln	Leu	Val	Trp	Thr	Gln	Ala	Ala	Gln	60	65	70	75
Thr	Ser	Glu	Leu	Asp	Ser	Asn	Glu	His	Leu	Lys	Thr	Phe	Ser		80	85	90	95
Tyr	Phe	Pro	Tyr	Pro	Ser	Leu	Ala	Asp	Ile	Ala	Leu	Leu	Cys	Leu	100	105	110	115
Arg	Tyr	Gly	Leu	Gln	Met	Glu	Lys	Val	Lys	Thr	Trp	Phe	Met	Ala	120	125	130	135
Gln	Arg	Leu	Arg	Cys	Gly	Ile	Ser	Trp	Ser	Ser	Glu	Glu	Ile	Glu	140	145	150	155
Glu	Thr	Arg	Ala	Arg	Val	Val	Tyr	Arg	Arg	Asp	Gln	Leu	His	Phe	160	165	170	175
Lys	Ser	Leu	Leu	Ser	Phe	Thr	His	His	Ala	Gly	Arg	Pro	Pro	Glu	180	185	190	195
Glu	Val	Pro	Pro	Pro	Pro	Val	Pro	Ala	Pro	Glu	Gln	Val	Gly	Ile	200	205	210	215
Gly	Ile	Gly	Pro	Pro	Thr	Leu	Ser	Lys	Pro	Thr	Gln	Thr	Lys	Gly	220	225	230	235
Leu	Lys	Val	Glu	Pro	Glu	Glu	Pro	Ser	Gln	Met	Pro	Pro	Leu	Pro	240	245	250	255
Gln	Ser	His	Gln	Lys	Leu	Lys	Glu	Ser	Leu	Met	Thr	Pro	Gly	Ser	260	265	270	275
Gly	Ala	Phe	Pro	Tyr	Gln	Ser	Asp	Phe	Trp	Gln	His	Leu	Gln	Ser	280	285	290	295
Ser	Gly	Leu	Ser	Lys	Glu	Gln	Ala	Gly	Arg	Gly	Pro	Asn	Gln	Ser	300	305	310	315
His	Gly	Ile	Gly	Thr	Ala	Ser	Trp	Asn	His	Ser	Thr	Thr	Val	Pro	320	325	330	335
Gln	Pro	Gln	Ala	Arg	Asp	Lys	Pro	Pro	Pro	Ile	Ala	Leu	Ile	Ala	340	345	350	355
Ser	Ser	Cys	Lys	Glu	Glu	Ser	Ala	Ser	Ser	Val	Thr	Pro	Ser	Ser	360	365	370	375
Ser	Ser	Thr	Ser	Ser	Ser	Phe	Gln	Val	Leu	Ala	Asn	Gly	Ala	Thr	380	385	390	395
Ala	Thr	Ser	Lys	Pro	Leu	Gln	Pro	Leu	Gly	Cys	Val	Pro	Gln	Ser	400			
Val	Ser	Pro	Ser	Glu	Gln	Ala	Leu	Pro	Pro	His	Leu	Glu	Pro	Ala				
Trp	Pro	Gln	Gly	Leu	Arg	His	Asn	Ser	Val	Pro	Gly	Arg	Val	Gly				
Pro	Thr	Glu	Tyr	Leu	Ser	Pro	Asp	Met	Gln	Arg	Gln	Arg	Lys	Thr				
Lys	Arg	Lys	Thr	Lys	Glu	Gln	Leu	Ala	Ile	Leu	Lys	Ser	Phe	Phe				
Leu	Gln	Cys	Gln	Trp	Ala	Arg	Arg	Glu	Asp	Tyr	Gln	Lys	Leu	Glu				
Gln	Ile	Thr	Gly	Leu	Pro	Arg	Pro	Glu	Ile	Ile	Gln	Trp	Phe	Gly				

Asp Thr Arg Tyr	Ala Leu Lys His Gly Gln Leu Lys Trp Phe Arg	
	410	420
Asp Asn Ala Val	Pro Gly Ala Pro Ser Phe Gln Asp Pro Ala Ile	
	425	435
Pro Thr Pro Pro	Pro Ser Thr Arg Ser Leu Asn Glu Arg Ala Glu	
	440	450
Thr Pro Pro Leu	Pro Ile Pro Pro Pro Pro Pro Asp Ile Gln Pro	
	455	465
Leu Glu Arg Tyr	Trp Ala Ala His Gln Gln Leu Arg Glu Thr Asp	
	470	480
Ile Pro Gln Leu	Ser Gln Ala Ser Arg Leu Ser Thr Gln Gln Val	
	485	495
Leu Asp Trp Phe	Asp Ser Arg Leu Pro Gln Pro Ala Glu Val Val	
	500	510
Val Cys Leu Asp	Glu Glu Glu Glu Glu Glu Glu Glu Glu Leu Pro	
	515	525
Glu Asp Asp Glu	Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Asp	
	530	540
Asp Asp Asp Asp	Asp Val Ile Ile Gln Asp	
	545	550

<210> 63

<211> 450

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2493052CD1

<400> 63

Met Ala Ala Ser Lys	Thr Gln Gly Ala Val Ala Arg Met Gln Glu	
1	5	10
Asp Arg Asp Gly Ser	Cys Ser Thr Val Gly Val Gly Tyr Gly	
	20	25
Asp Ser Lys Asp Cys	Ile Leu Glu Pro Leu Ser Leu Pro Glu Ser	
	35	40
Pro Gly Gly Thr Thr	Thr Leu Glu Gly Ser Pro Ser Val Pro Cys	
	50	55
Ile Phe Cys Glu Glu	His Phe Pro Val Ala Glu Gln Asp Lys Leu	
	65	70
Leu Lys His Met Ile	Ile Glu His Lys Ile Val Ile Ala Asp Val	
	80	85
Lys Leu Val Ala Asp	Phe Gln Arg Tyr Ile Leu Tyr Trp Arg Lys	
	95	100
Arg Phe Thr Glu Gln	Pro Ile Thr Asp Phe Cys Ser Val Ile Arg	
	110	115
Ile Asn Ser Thr Ala	Pro Phe Glu Glu Gln Glu Asn Tyr Phe Leu	
	125	130
Leu Cys Asp Val Leu	Pro Glu Asp Arg Ile Leu Arg Glu Glu Leu	
	140	145
Gln Lys Gln Arg Leu	Arg Glu Ile Leu Glu Gln Gln Gln Gln Glu	
	155	160
Arg Asn Asp Thr Asn	Phe His Gly Val Cys Met Phe Cys Asn Glu	
	170	175
Glu Phe Leu Gly Asn	Arg Ser Val Ile Leu Asn His Met Ala Arg	
	185	190
Glu His Ala Phe Asn	Ile Gly Leu Pro Asp Asn Ile Val Asn Cys	
	200	205
Asn Glu Phe Leu Cys	Thr Leu Gln Lys Lys Leu Asp Asn Leu Gln	
	215	220
Cys Leu Tyr Cys Glu	Lys Thr Phe Arg Asp Lys Asn Thr Leu Lys	
	230	235

Asp	His	Met	Arg	Lys	Lys	Gln	His	Arg	Lys	Ile	Asn	Pro	Lys	Asn	
				245					250					255	
Arg	Glu	Tyr	Asp	Arg	Phe	Tyr	Val	Ile	Asn	Tyr	Leu	Glu	Leu	Gly	
				260					265					270	
Lys	Ser	Trp	Glu	Glu	Val	Gln	Leu	Glu	Asp	Asp	Arg	Glu	Leu	Leu	
				275					280					285	
Asp	His	Gln	Glu	Asp	Asp	Trp	Ser	Asp	Trp	Glu	Glu	His	Pro	Ala	
				290					295					300	
Ser	Ala	Val	Cys	Leu	Phe	Cys	Glu	Lys	Gln	Ala	Glu	Thr	Ile	Glu	
				305					310					315	
Lys	Leu	Tyr	Val	His	Met	Glu	Asp	Ala	His	Glu	Phe	Asp	Leu	Leu	
				320					325					330	
Lys	Ile	Lys	Ser	Glu	Leu	Gly	Leu	Asn	Phe	Tyr	Gln	Gln	Val	Lys	
				335					340					345	
Leu	Val	Asn	Phe	Ile	Arg	Arg	Gln	Val	His	Gln	Cys	Arg	Cys	Tyr	
				350					355					360	
Gly	Cys	His	Val	Lys	Phe	Lys	Ser	Lys	Ala	Asp	Leu	Arg	Thr	His	
				365					370					375	
Met	Glu	Glu	Thr	Lys	His	Thr	Ser	Leu	Leu	Pro	Asp	Arg	Lys	Thr	
				380					385					390	
Trp	Asp	Gln	Leu	Glu	Tyr	Tyr	Phe	Pro	Thr	Tyr	Glu	Asn	Asp	Thr	
				395					400					405	
Leu	Leu	Cys	Thr	Leu	Ser	Asp	Ser	Glu	Ser	Asp	Leu	Thr	Ala	Gln	
				410					415					420	
Glu	Gln	Asn	Glu	Asn	Val	Pro	Ile	Ile	Ser	Glu	Asp	Thr	Ser	Lys	
				425					430					435	
Leu	Tyr	Ala	Leu	Lys	Gln	Ser	Ser	Ile	Leu	Asn	Gln	Leu	Leu	Leu	
				440					445					450	

<210> 64

<211> 378

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2512074CD1

<400> 64

Met	Ile	Ser	Phe	Gln	Glu	Ser	Val	Thr	Phe	Gln	Asp	Val	Ala	Val	
1				5					10					15	
Asp	Phe	Thr	Ala	Glu	Glu	Trp	Gln	Leu	Leu	Asp	Cys	Ala	Glu	Arg	
				20					25					30	
Thr	Leu	Tyr	Trp	Asp	Val	Met	Leu	Glu	Asn	Tyr	Arg	Asn	Leu	Ile	
				35					40					45	
Ser	Val	Gly	Cys	Pro	Ile	Thr	Lys	Thr	Lys	Val	Ile	Leu	Lys	Val	
				50					55					60	
Glu	Gln	Gly	Gln	Pro	Trp	Met	Val	Glu	Gly	Ala	Asn	Pro	His		
				65					70					75	
Glu	Ser	Ser	Pro	Glu	Ser	Asp	Tyr	Pro	Leu	Val	Asp	Glu	Pro	Gly	
				80					85					90	
Lys	His	Arg	Glu	Ser	Lys	Asp	Asn	Phe	Leu	Lys	Ser	Val	Leu	Leu	
				95					100					105	
Thr	Phe	Asn	Lys	Ile	Leu	Thr	Met	Glu	Arg	Ile	His	His	Tyr	Asn	
				110					115					120	
Met	Ser	Thr	Ser	Leu	Asn	Pro	Met	Arg	Lys	Lys	Ser	Tyr	Lys	Ser	
				125					130					135	
Phe	Glu	Lys	Cys	Leu	Pro	Pro	Asn	Leu	Asp	Leu	Leu	Lys	Tyr	Asn	
				140					145					150	
Arg	Ser	Tyr	Thr	Val	Glu	Asn	Ala	Tyr	Glu	Cys	Ser	Glu	Cys	Gly	
				155					160					165	
Lys	Ala	Phe	Lys	Lys	Lys	Phe	His	Phe	Ile	Arg	His	Glu	Lys	Asn	

His Thr Arg Lys	170	Pro Phe Glu Cys	175	Asn Asp Cys Gly Lys	180
	185		190		195
Tyr Ser Arg Lys	200	Ala His Leu Ala Thr	205	His Gln Lys Ile His	210
Gly Glu Arg Pro	215	Phe Val Cys Asn Asp	220	Cys Gly Lys Ala Phe	225
His Lys Ala Gln	230	Leu Val Val His Gln	235	Arg Leu His Thr Gly	240
Lys Pro Tyr Glu	245	Cys Ser Gln Cys Gly	250	Lys Thr Phe Thr Trp	255
Ser Ser Phe Asn	260	Gln His Val Lys Ser	265	His Thr Leu Glu Lys	270
Phe Glu Cys Lys	275	Glu Cys Gly Lys Thr	280	Phe Arg Tyr Ser Ser	285
Leu Tyr Lys His	290	Ser Arg Phe His Thr	295	Gly Glu Lys Pro Tyr	300
Cys Ile Ile Cys	305	Gly Lys Ala Phe Gly	310	Asn Thr Ser Val Leu	315
Thr His Gln Arg	320	Ile His Thr Gly Glu	325	Lys Pro Tyr Ser Cys	330
Glu Cys Gly Lys	335	Ala Phe Ile Lys Lys	340	Ser His Leu Leu Arg	345
Gln Ile Thr His	350	Thr Gly Glu Lys Pro	355	Tyr Glu Cys Asn Arg	360
Gly Lys Ala Phe	365	Ser Gln Lys Ser Asn	370	Leu Ile Val His Gln	375
Ile His Thr					

<210> 65

<211> 233

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2646274CD1

<400> 65

Met Pro Ile Leu Val	1	Glu Lys Phe Pro	10	Phe Val Arg Lys Ser	15
Arg Thr Leu Glu Cys	20	Tyr Val His Asn	25	Leu Leu Arg Ile Ser	30
Tyr Phe Pro Thr Leu	35	Arg His Glu Ile	40	Leu Glu Leu Ile Ile	45
Lys Leu Leu Lys Leu	50	Asp Val Asn Ala	55	Ser Arg Gln Gly Ile	60
Asp Ala Glu Glu Thr	65	Ala Asn Gln Thr	70	Cys Gly Gly Thr Asp	75
Thr Glu Gly Leu Phe	80	Asn Met Gly Phe	85	Ala Glu Ala Phe Leu	90
His Leu Trp Lys Asn	95	Leu Gln Asp Pro	100	Ser Asn Pro Ala Ile	105
Arg Gln Ala Ala Gly	110	Asn Tyr Ile Gly	115	Ser Phe Leu Ala Arg	120
Lys Phe Ile Ser Leu	125	Ile Thr Val Lys	130	Pro Cys Leu Asp Leu	135
Val Asn Trp Leu His	140	Ile Tyr Leu Asn	145	Gln Asp Ser Gly Thr	150
Lys Ala Phe Cys Asp	155	Val Ala Leu His	160	Gly Pro Phe Tyr Ser	165
Cys Gln Ala Val Phe		Tyr Thr Phe Val		Phe Arg His Lys Gln	Leu

Leu Ser Gly Asn	170	Leu Lys Glu Gly	175	Leu Gln Tyr Pro Gln Ser	180
	185		190		195
Asn Phe Glu Arg	200	Ile Val Met Ser Gln	205	Leu Asn Pro Leu Lys	210
	215	Val Val Asn Phe Phe	220	Ala Ala Ile Thr Lys	225
Cys Leu Pro Ser					
Lys Thr Cys Gly	230	Tyr Gly Trp Trp			

<210> 66
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2672566CD1

Met Leu Ser Val	Asp	Met Glu Asn Lys	Glu Asn Gly Ser Val	Gly
1	5		10	15
Val Lys Asn Ser	Met Glu Asn Gly Arg	Pro Asp Pro Ala	Asp	
	20		25	30
Trp Ala Val Met	Asp Val Val Asn Tyr	Phe Arg Thr Val	Gly Phe	
	35		40	45
Glu Glu Gln Ala	Ser Ala Phe Gln Glu	Gln Glu Ile Asp	Gly Lys	
	50		55	60
Ser Leu Leu Leu	Met Thr Arg Asn Asp	Val Leu Thr Gly	Leu Gln	
	65		70	75
Leu Lys Leu Gly	Pro Ala Leu Lys Ile	Tyr Glu Tyr His	Val Lys	
	80		85	90
Pro Leu Gln Thr	Lys His Leu Lys Asn	Asn Ser Ser		
	95		100	

<210> 67
 <211> 287
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2689674CD1

Met Ala Ala Ser	Leu Trp Met Gly Asp	Leu Glu Pro Tyr Met	Asp
1	5	10	15
Glu Asn Phe Ile	Ser Arg Ala Phe Ala	Thr Met Gly Glu Thr	Val
	20	25	30
Met Ser Val Lys	Ile Ile Arg Asn Arg	Leu Thr Gly Ile Pro	Ala
	35	40	45
Gly Tyr Cys Phe	Val Glu Phe Ala Asp	Leu Ala Thr Ala Glu	Lys
	50	55	60
Cys Leu His Lys	Ile Asn Gly Lys Pro	Leu Pro Gly Ala Thr	Pro
	65	70	75
Ala Lys Arg Phe	Lys Leu Asn Tyr Ala	Thr Tyr Gly Lys Gln	Pro
	80	85	90
Asp Asn Ser Pro	Glu Tyr Ser Leu Phe	Val Gly Asp Leu Thr	Pro
	95	100	105
Asp Val Asp Asp	Gly Met Leu Tyr Glu	Phe Phe Val Lys Val	Tyr
	110	115	120
Pro Ser Cys Arg	Gly Gly Lys Val Val	Leu Asp Gln Thr Gly	Val
	125	130	135

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Ser Lys Gly Tyr Gly Phe Val Lys Phe Thr Asp Glu Leu Glu Gln
140 145 150
Lys Arg Ala Leu Thr Glu Cys Gln Gly Ala Val Gly Leu Gly Ser
155 160 165
Lys Pro Val Arg Leu Ser Val Ala Ile Pro Lys Ala Ser Arg Val
170 175 180
Lys Pro Val Glu Tyr Ser Gln Met Tyr Ser Tyr Ser Tyr Asn Gln
185 190 195
Tyr Tyr Gln Gln Tyr Gln Asn Tyr Tyr Ala Gln Trp Gly Tyr Asp
200 205 210
Gln Asn Thr Gly Ser Tyr Ser Tyr Ser Tyr Pro Gln Tyr Gly Tyr
215 220 225
Thr Gln Ser Thr Met Gln Thr Tyr Glu Glu Val Gly Asp Asp Ala
230 235 240
Leu Glu Asp Pro Met Pro Gln Leu Asp Val Thr Glu Ala Asn Lys
245 250 255
Glu Phe Met Glu Gln Ser Glu Glu Leu Tyr Asp Ala Leu Met Asp
260 265 270
Cys His Trp Gln Pro Leu Asp Thr Val Ser Ser Glu Ile Pro Ala
275 280 285
Met Met

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<210> 68
 <211> 208
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2703282CD1

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<400> 68
Met Lys Lys Asn Glu Val Tyr Glu Thr Phe Ser Tyr Pro Glu Ser
1 5 10 15
Tyr Ser Pro Thr Leu Pro Val Ser Arg Arg Glu Asn Asn Ser Pro
20 25 30
Ser Asn Leu Pro Arg Pro Ser Phe Cys Met Glu Glu Tyr Gln Arg
35 40 45
Ala Glu Leu Glu Glu Asp Pro Ile Leu Ser Arg Thr Pro Ser Pro
50 55 60
Val His Pro Ser Asp Phe Ser Glu His Asn Cys Gln Pro Tyr Tyr
65 70 75
Ala Ser Asp Gly Ala Thr Tyr Gly Ser Ser Gly Leu Cys Leu
80 85 90
Gly Asn Pro Arg Ala Asp Ser Ile His Asn Thr Tyr Ser Thr Asp
95 100 105
His Ala Ser Ala Ala Pro Pro Ser Val Thr Arg Ser Pro Val Glu
110 115 120
Asn Asp Gly Tyr Ile Glu Glu Gly Ser Ile Thr Lys His Pro Ser
125 130 135
Thr Trp Ser Val Glu Ala Val Val Leu Phe Leu Lys Gln Thr Asp
140 145 150
Pro Leu Ala Leu Cys Pro Leu Val Asp Leu Phe Arg Ser His Glu
155 160 165
Ile Asp Gly Lys Ala Leu Leu Leu Leu Thr Ser Asp Val Leu Leu
170 175 180
Lys His Leu Gly Val Lys Leu Gly Thr Ala Val Lys Leu Cys Tyr
185 190 195
Tyr Ile Asp Arg Leu Lys Gln Gly Lys Cys Phe Glu Asn
200 205

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<210> 69

<211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2738293CD1

<400> 69
 Met Ser Lys Leu Ser Phe Arg Ala Arg Ala Leu Asp Ala Ala Lys
 1 5 10 15
 Pro Leu Pro Ile Tyr Arg Gly Lys Asp Met Pro Asp Leu Asn Asp
 20 25 30
 Cys Val Ser Ile Asn Arg Ala Val Pro Gln Met Pro Thr Gly Met
 35 40 45
 Glu Lys Glu Glu Glu Ser Glu His His Leu Gln Arg Ala Ile Ser
 50 55 60
 Ala Gln Gln Val Phe Arg Glu Lys Lys Glu Ser Met Val Ile Pro
 65 70 75
 Val Pro Glu Ala Glu Ser Asn Val Asn Tyr Tyr Asn Arg Leu Tyr
 80 85 90
 Lys Gly Glu Phe Lys Gln Pro Lys Gln Phe Ile His Ile Gln Arg
 95 100 105
 Ile Trp Gly His Tyr Gln Pro Glu Thr Thr Leu Lys Phe Leu Leu
 110 115 120
 Val Cys Phe Val His Leu Phe Leu Asp His Ser Ile Ser Phe Asn
 125 130 135
 Leu Gly Cys Arg Ser Ala Gln Gly Ser Val Leu Arg Lys Ile Phe
 140 145 150
 Cys Phe Ser Phe Leu Pro Lys Gly Lys Leu Arg Asn Thr Lys Phe
 155 160 165
 Phe Ala Phe Pro Phe Cys Met Ala Asn Leu Phe Leu
 170 175

<210> 70
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2772776CD1

<400> 70
 Met Ala Ala Thr Glu Pro Ile Leu Ala Ala Thr Gly Ser Pro Ala
 1 5 10 15
 Ala Val Pro Pro Glu Lys Leu Glu Gly Ala Gly Ser Ser Ser Ala
 20 25 30
 Pro Glu Arg Asn Cys Val Gly Ser Ser Leu Pro Glu Ala Ser Pro
 35 40 45
 Pro Ala Pro Glu Pro Ser Ser Pro Asn Ala Ala Val Pro Glu Ala
 50 55 60
 Ile Pro Thr Pro Arg Ala Ala Ala Ser Ala Ala Leu Glu Leu Pro
 65 70 75
 Leu Gly Pro Ala Pro Val Ser Val Ala Pro Gln Ala Glu Ala Glu
 80 85 90
 Ala Arg Ser Thr Pro Gly Pro Ala Gly Ser Arg Leu Gly Pro Glu
 95 100 105
 Thr Phe Arg Gln Arg Phe Arg Gln Phe Arg Tyr Gln Asp Ala Ala
 110 115 120
 Gly Pro Arg Glu Ala Phe Arg Gln Leu Arg Glu Leu Ser Arg Gln
 125 130 135
 Trp Leu Arg Pro Asp Ile Arg Thr Lys Glu Gln Ile Val Glu Met

	140		145		150
Leu Val Gln Glu	Gln Leu Leu Ala Ile	Leu Pro Glu Ala Ala	Arg		
	155		160		165
Ala Arg Arg Ile	Arg Arg Arg Thr Asp	Val Arg Ile Thr Gly			
	170		175		

<210> 71
 <211> 212
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2774476CD1

<400> 71
 Met Asp Pro Ala Gly Ala Ala Asp Pro Ser Val Pro Pro Asn Pro
 1 5 10 15
 Leu Thr His Leu Ser Leu Gln Asp Arg Ser Glu Met Gln Leu Gln
 20 25 30
 Ser Glu Ala Asp Arg Arg Ser Leu Pro Gly Thr Trp Thr Arg Ser
 35 40 45
 Ser Pro Glu His Thr Thr Ile Leu Arg Gly Gly Val Arg Arg Cys
 50 55 60
 Leu Gln Gln Gln Cys Glu Gln Thr Val Arg Ile Leu His Ala Lys
 65 70 75
 Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys Arg Phe Phe Cys Pro
 80 85 90
 Pro Pro Cys Val Tyr Leu Ser Gly Pro Gly Trp Arg Val Lys Pro
 95 100 105
 Gly Gln Asp Gln Ala His Gln Ala Gly Glu Thr Gly Pro Thr Val
 110 115 120
 Cys Gly Tyr Met Gly Leu Asp Ser Ala Ser Gly Ser Ala Thr Glu
 125 130 135
 Thr Gln Lys Leu Asn Phe Glu Gln Gln Pro Asp Ser Arg Glu Phe
 140 145 150
 Gly Cys Ala Lys Thr Leu Tyr Ile Ser Asp Ala Asp Lys Arg Lys
 155 160 165
 His Phe Arg Leu Val Leu Arg Leu Val Leu Arg Gly Gly Arg Glu
 170 175 180
 Leu Gly Thr Phe His Ser Arg Leu Ile Lys Val Ile Ser Lys Pro
 185 190 195
 Ser Gln Lys Lys Gln Ser Leu Lys Asn Thr Asp Arg Glu Gln Gly
 200 205 210
 Gly Ala

<210> 72
 <211> 256
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2804624CD1

<400> 72
 Met Lys Leu Leu Glu Asn Ser Ser Phe Glu Ala Ile Asn Ser Gln
 1 5 10 15
 Leu Thr Val Glu Thr Gly Asp Ala His Ile Ile Gly Arg Ile Glu
 20 25 30
 Ser Tyr Ser Cys Lys Met Ala Gly Asp Asp Lys His Met Phe Lys
 35 40 45

Gln Phe Cys Gln Glu Gly Gln Pro His Val Leu Glu Ala Leu Ser
 50 55 60
 Pro Pro Gln Thr Ser Gly Leu Ser Pro Ser Arg Leu Ser Lys Ser
 65 70 75
 Gln Gly Gly Glu Glu Glu Gly Pro Leu Ser Asp Lys Cys Ser Arg
 80 85 90
 Lys Thr Leu Phe Tyr Leu Ile Ala Thr Leu Asn Glu Ser Phe Arg
 95 100 105
 Pro Asp Tyr Asp Phe Ser Thr Ala Arg Ser His Glu Phe Ser Arg
 110 115 120
 Glu Pro Ser Leu Ser Trp Val Val Asn Ala Val Asn Cys Ser Leu
 125 130 135
 Phe Ser Ala Val Arg Glu Asp Phe Lys Asp Leu Lys Pro Gln Leu
 140 145 150
 Trp Asn Ala Val Asp Glu Glu Ile Cys Leu Ala Glu Cys Asp Ile
 155 160 165
 Tyr Ser Tyr Asn Pro Asp Leu Asp Ser Asp Pro Phe Gly Glu Asp
 170 175 180
 Gly Ser Leu Trp Ser Phe Asn Tyr Phe Phe Tyr Asn Lys Arg Leu
 185 190 195
 Lys Arg Ile Val Phe Phe Ser Cys Arg Ser Ile Ser Gly Ser Thr
 200 205 210
 Tyr Thr Pro Ser Glu Ala Gly Asn Glu Leu Asp Met Glu Leu Gly
 215 220 225
 Glu Glu Glu Val Glu Glu Glu Ser Arg Ser Arg Gly Ser Gly Ala
 230 235 240
 Glu Glu Thr Ser Thr Met Glu Glu Asp Arg Val Pro Val Ile Cys
 245 250 255
 Ile

<210> 73

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2848225CD1

<400> 73

Met Asp Ala Val Ala Phe Glu Asp Val Ala Val Asn Phe Thr Gln
 1 5 10 15
 Glu Glu Trp Ala Leu Leu Gly Pro Ser Gln Lys Asn Leu Tyr Arg
 20 25 30
 Tyr Val Met Gln Glu Thr Ile Arg Asn Leu Asp Cys Ile Arg Met
 35 40 45
 Ile Trp Glu Glu Gln Asn Thr Glu Asp Gln Tyr Lys Asn Pro Arg
 50 55 60
 Arg Asn Leu Arg Cys His Met Val Glu Arg Phe Ser Glu Ser Lys
 65 70 75
 Asp Ser Ser Gln Cys Gly Glu Thr Phe Ser Leu Ile Arg Asp Ser
 80 85 90
 Ile Val Asn Asn Ser Ile Cys Pro Gly Glu Asp Pro Cys Gln Ser
 95 100 105
 Ala Glu Cys Glu Glu Val Ile Met Gly His Leu Ser Leu Asn Ser
 110 115 120
 His Ile Arg Val Asp Ser Gly His Lys Pro His Glu Tyr Gln Glu
 125 130 135
 Tyr Gly Glu Lys Pro His Thr His Lys Gln Arg Gly Lys Ala Phe
 140 145 150
 Ser Tyr His His Ser Phe Gln Ser Arg Gly Arg Pro His Thr Gly
 155 160 165

Lys	Lys	Arg	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Thr	Phe	Ser	Ser	
				170					175					180	
Arg	Arg	Asn	Leu	Arg	Arg	His	Met	Val	Val	Gln	Gly	Gly	Asn	Arg	
				185					190					195	
Pro	Tyr	Lys	Cys	Lys	Leu	Cys	Gly	Lys	Ala	Phe	Phe	Trp	Pro	Ser	
				200					205					210	
Leu	Leu	Arg	Met	His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	
				215					220					225	
Glu	Cys	Lys	Gln	Cys	Ser	Lys	Ala	Phe	Pro	Phe	Tyr	Ser	Ser	Tyr	
				230					235					240	
Arg	Arg	His	Glu	Arg	Met	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	
				245					250					255	
Lys	Gln	Cys	Ser	Lys	Ala	Leu	Pro	Asp	Ser	Ser	Ser	Tyr	Ile	Arg	
				260					265					270	
His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Thr	Cys	Lys	Gln	
				275					280					285	
Cys	Gly	Lys	Ala	Phe	Ser	Val	Ser	Ser	Ser	Leu	Arg	Arg	His	Glu	
				290					295					300	
Thr	Thr	His	Ser	Ala	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys	Gly	
				305					310					315	
Lys	Thr	Phe	His	His	Leu	Gly	Ser	Phe	Gln	Ile	His	Met	Lys	Arg	
				320					325					330	
His	Thr	Gly	Asp	Arg	Pro	His	Lys	Cys	Lys	Ile	Cys	Gly	Lys	Gly	
				335					340					345	
Phe	Asp	Pro	Ser	Leu	Val	Arg	Tyr	His	Glu	Arg	Ile	His	Thr	Gly	
				350					355					360	
Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Thr	Leu	Ser	His	
				365					370					375	
Ser	Ser	Ser	Phe	Arg	Arg	His	Met	Ile	Met	His	Thr	Gly	Gly	Gly	
				380					385					390	
Pro	His	Lys	Cys	Lys	Ile	Cys	Gly	Lys	Ala	Phe	Val	Tyr	Pro	Ser	
				395					400					405	
Val	Cys	Gln	Arg	His	Glu	Lys	Ser	His	Ser	Gly	Glu	Lys	Pro	Tyr	
				410					415					420	
Glu	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Leu	Ser	His	Ser	Ser	Ser	Phe	
				425					430					435	
Arg	Arg	His	Met	Val	Met	His	Thr	Gly	Asp	Gly	Pro	Asn	Lys	Cys	
				440					445					450	
Lys	Val	Cys	Gly	Lys	Ala	Phe	Val	Tyr	Pro	Ser	Val	Cys	Gln	Arg	
				455					460					465	
His	Glu	Lys	Thr	His	Trp	Arg	Glu	Thr	Ile						
				470					475						

<210> 74

<211> 206

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2882241CD1

<400> 74

Met	Glu	Pro	Leu	Ala	Ser	Asn	Ile	Gln	Val	Leu	Leu	Gln	Ala	Ala	
1				5					10					15	
Glu	Phe	Leu	Glu	Arg	Arg	Glu	Arg	Glu	Ala	Glu	His	Gly	Tyr	Ala	
				20					25					30	
Ser	Leu	Cys	Pro	His	Arg	Ser	Pro	Gly	Pro	Ile	His	Arg	Arg	Lys	
				35					40					45	
Lys	Arg	Pro	Pro	Gln	Ala	Pro	Gly	Ala	Gln	Asp	Ser	Gly	Arg	Ser	
				50					55					60	
Val	His	Asn	Glu	Leu	Glu	Lys	Arg	Arg	Arg	Ala	Gln	Leu	Lys	Arg	
				65					70					75	

Cys	Leu	Glu	Arg	Leu	Lys	Gln	Gln	Met	Pro	Leu	Gly	Ala	Asp	Cys	
				80					85					90	
Ala	Arg	Tyr	Thr	Thr	Leu	Ser	Leu	Leu	Arg	Arg	Ala	Arg	Met	His	
				95					100					105	
Ile	Gln	Lys	Leu	Glu	Asp	Gln	Glu	Gln	Arg	Ala	Arg	Gln	Leu	Lys	
				110					115					120	
Glu	Arg	Leu	Arg	Ser	Lys	Gln	Gln	Ser	Leu	Gln	Arg	Gln	Leu	Glu	
				125					130					135	
Gln	Leu	Arg	Gly	Leu	Ala	Gly	Ala	Ala	Glu	Arg	Glu	Arg	Leu	Arg	
				140					145					150	
Ala	Asp	Ser	Leu	Asp	Ser	Ser	Gly	Leu	Ser	Ser	Glu	Arg	Ser	Asp	
				155					160					165	
Ser	Asp	Gln	Glu	Glu	Leu	Glu	Val	Asp	Val	Glu	Ser	Leu	Val	Phe	
				170					175					180	
Gly	Gly	Glu	Ala	Glu	Leu	Leu	Arg	Gly	Phe	Val	Ala	Gly	Gln	Glu	
				185					190					195	
His	Ser	Tyr	Ser	His	Gly	Gly	Gly	Ala	Trp	Leu					
				200					205						

<210> 75

<211> 596

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2939011CD1

<400> 75

Met	Arg	Arg	Asn	Lys	Gly	Asp	Ile	Lys	Glu	Phe	Trp	Pro	Gln	Gln	
1				5					10					15	
Ser	Gln	Leu	Ser	Asp	Phe	Met	Lys	Met	Ala	Asn	Ala	Glu	Val	Ser	
				20					25					30	
Val	Pro	Val	Gly	Asp	Val	Val	Val	Val	Pro	Thr	Glu	Gly	Asn	Glu	
				35					40					45	
Gly	Glu	Asn	Pro	Glu	Asp	Thr	Lys	Thr	Gln	Val	Ile	Leu	Gln	Leu	
				50					55					60	
Gln	Pro	Val	Gln	Gln	Gly	Leu	Phe	Ile	Asp	Gly	His	Phe	Tyr	Asn	
				65					70					75	
Arg	Ile	Tyr	Glu	Ala	Gly	Ser	Glu	Asn	Asn	Thr	Ala	Val	Val	Ala	
				80					85					90	
Val	Glu	Thr	His	Thr	Ile	His	Lys	Ile	Glu	Glu	Gly	Ile	Asp	Thr	
				95					100					105	
Gly	Thr	Ile	Glu	Ala	Asn	Glu	Asp	Met	Glu	Ile	Ala	Tyr	Pro	Ile	
				110					115					120	
Thr	Cys	Gly	Glu	Ser	Lys	Ala	Ile	Leu	Leu	Trp	Lys	Lys	Phe	Val	
				125					130					135	
Cys	Pro	Gly	Ile	Asn	Val	Lys	Cys	Val	Lys	Phe	Asn	Asp	Gln	Leu	
				140					145					150	
Ile	Ser	Pro	Lys	His	Phe	Val	His	Leu	Ala	Gly	Lys	Ser	Thr	Leu	
				155					160					165	
Lys	Asp	Trp	Lys	Arg	Ala	Ile	Arg	Leu	Gly	Gly	Ile	Met	Leu	Arg	
				170					175					180	
Lys	Met	Met	Asp	Ser	Gly	Gln	Ile	Asp	Phe	Tyr	Gln	His	Asp	Lys	
				185					190					195	
Val	Cys	Ser	Asn	Thr	Cys	Arg	Ser	Thr	Lys	Phe	Asp	Leu	Leu	Ile	
				200					205					210	
Ser	Ser	Ala	Arg	Ala	Pro	Val	Pro	Gly	Gln	Gln	Thr	Ser	Val	Val	
				215					220					225	
Gln	Thr	Pro	Thr	Ser	Ala	Asp	Gly	Ser	Ile	Thr	Gln	Ile	Ala	Ile	
				230					235					240	
Ser	Glu	Glu	Ser	Met	Glu	Glu	Ala	Gly	Leu	Glu	Trp	Asn	Ser	Ala	
				245					250					255	

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Leu Thr Ala Ala Val Thr Met Ala Thr Glu Glu Gly Val Lys Lys
260 265 270
Asp Ser Glu Glu Ile Ser Glu Asp Thr Leu Met Phe Trp Lys Gly
275 280 285
Ile Ala Asp Val Gly Leu Met Glu Glu Val Val Cys Asn Ile Gln
290 295 300
Lys Glu Ile Glu Glu Leu Leu Arg Gly Val Gln Gln Arg Leu Ile
305 310 315
Gln Ala Pro Phe Gln Val Thr Asp Ala Ala Val Leu Asn Asn Val
320 325 330
Ala His Thr Phe Gly Leu Met Asp Thr Val Lys Lys Val Leu Asp
335 340 345
Asn Arg Arg Asn Gln Val Glu Gln Gly Glu Glu Gln Phe Leu Tyr
350 355 360
Thr Leu Thr Asp Leu Glu Arg Gln Leu Glu Glu Gln Lys Lys Gln
365 370 375
Gly Gln Asp His Arg Leu Lys Ser Gln Thr Val Gln Asn Val Val
380 385 390
Leu Met Pro Val Ser Thr Pro Lys Pro Pro Lys Arg Pro Arg Leu
395 400 405
Gln Arg Pro Ala Ser Thr Thr Val Leu Ser Pro Ser Pro Pro Val
410 415 420
Gln Gln Pro Gln Phe Thr Val Ile Ser Pro Ile Thr Ile Thr Pro
425 430 435
Val Gly Gln Ser Phe Ser Met Gly Asn Ile Pro Val Ala Thr Leu
440 445 450
Ser Gln Gly Ser Ser Pro Val Thr Val His Thr Leu Pro Ser Gly
455 460 465
Pro Gln Leu Phe Arg Tyr Ala Thr Val Val Ser Ser Ala Lys Ser
470 475 480
Ser Ser Pro Asp Thr Val Thr Ile His Pro Ser Ser Ser Leu Ala
485 490 495
Leu Leu Ser Ser Thr Ala Met Gln Asp Gly Ser Thr Leu Gly Asn
500 505 510
Met Thr Thr Met Val Ser Pro Val Glu Leu Val Ala Met Glu Ser
515 520 525
Gly Leu Thr Ser Ala Ile Gln Ala Val Glu Ser Thr Ser Glu Asp
530 535 540
Gly Gln Thr Ile Ile Glu Ile Asp Pro Ala Pro Asp Pro Glu Ala
545 550 555
Glu Asp Thr Glu Gly Lys Ala Val Ile Leu Glu Thr Glu Leu Arg
560 565 570
Thr Glu Glu Lys Val Val Ala Glu Met Glu Glu His Gln His Gln
575 580 585
Val His Asn Val Glu Ile Val Val Leu Glu Asp
590 595

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<210> 76

<211> 644

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2947188CD1

<400> 76

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Met Leu Glu Asn Tyr Gly Asn Val Ala Ser Leu Gly Phe Pro Leu
1 5 10 15
Leu Lys Pro Ala Val Ile Ser Gln Leu Glu Gly Gly Gly Glu Leu
20 25 30
Gly Gly Ser Ser Pro Leu Ala Ala Gly Thr Gly Leu Gln Gly Leu
35 40 45

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Gln	Thr	Val	Asp	Ile	Gln	Thr	Asp	Asn	Asp	Leu	Thr	Lys	Glu	Met
				50					55					60
Tyr	Glu	Gly	Lys	Glu	Asn	Val	Ser	Phe	Glu	Leu	Gln	Arg	Asp	Phe
				65					70					75
Ser	Gln	Glu	Thr	Asp	Phe	Ser	Glu	Ala	Ser	Leu	Leu	Glu	Lys	Gln
				80					85					90
Gln	Glu	Val	His	Ser	Ala	Gly	Asn	Ile	Lys	Lys	Glu	Lys	Ser	Asn
				95					100					105
Thr	Ile	Asp	Gly	Thr	Val	Lys	Asp	Glu	Thr	Ser	Pro	Val	Glu	Glu
				110					115					120
Cys	Phe	Phe	Ser	Gln	Ser	Ser	Asn	Ser	Tyr	Gln	Cys	His	Thr	Ile
				125					130					135
Thr	Gly	Glu	Gln	Pro	Ser	Gly	Cys	Thr	Gly	Leu	Gly	Lys	Ser	Ile
				140					145					150
Ser	Phe	Asp	Thr	Lys	Leu	Val	Lys	His	Glu	Ile	Ile	Asn	Ser	Glu
				155					160					165
Glu	Arg	Pro	Phe	Lys	Cys	Glu	Glu	Leu	Val	Glu	Pro	Phe	Arg	Cys
				170					175					180
Asp	Ser	Gln	Leu	Ile	Gln	His	Gln	Glu	Asn	Asn	Thr	Glu	Glu	Lys
				185					190					195
Pro	Tyr	Gln	Cys	Ser	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Ile	Asn	Glu
				200					205					210
Lys	Leu	Ile	Trp	His	Gln	Arg	Leu	His	Ser	Gly	Glu	Lys	Pro	Phe
				215					220					225
Lys	Cys	Val	Glu	Cys	Gly	Lys	Ser	Phe	Ser	Tyr	Ser	Ser	His	Tyr
				230					235					240
Ile	Thr	His	Gln	Thr	Ile	His	Ser	Gly	Glu	Lys	Pro	Tyr	Gln	Cys
				245					250					255
Lys	Met	Cys	Gly	Lys	Ala	Phe	Ser	Val	Asn	Gly	Ser	Leu	Ser	Arg
				260					265					270
His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Glu
				275					280					285
Cys	Gly	Asn	Gly	Phe	Ser	Cys	Ser	Ser	Ala	Tyr	Ile	Thr	His	Gln
				290					295					300
Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Asp	Cys	Gly
				305					310					315
Lys	Ala	Phe	Asn	Val	Asn	Ala	Lys	Leu	Ile	Gln	His	Gln	Arg	Ile
				320					325					330
His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	Gly	Lys	Gly
				335					340					345
Phe	Arg	Cys	Ser	Ser	Gln	Leu	Arg	Gln	His	Gln	Ser	Ile	His	Thr
				350					355					360
Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Glu	Cys	Gly	Lys	Gly	Phe	Asn
				365					370					375
Asn	Asn	Thr	Lys	Leu	Ile	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Glu
				380					385					390
Lys	Pro	Tyr	Glu	Cys	Thr	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Val	Lys
				395					400					405
Gly	Lys	Leu	Ile	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro
				410					415					420
Tyr	Glu	Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	Arg	Cys	Asn	Ser	Gln
				425					430					435
Phe	Arg	Gln	His	Leu	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu
				440					445					450
Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Val	Asn	Gly	Lys	Leu	Met
				455					460					465
Arg	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Phe	Glu	Cys	Asn
				470					475					480
Glu	Cys	Gly	Arg	Cys	Phe	Thr	Ser	Lys	Arg	Asn	Leu	Leu	Asp	His
				485					490					495
His	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Glu	Cys
				500					505					510
Gly	Lys	Ala	Phe	Ser	Ile	Asn	Ala	Lys	Leu	Thr	Arg	His	Gln	Arg

Ile His Thr Gly	515	520	525
Lys Pro Phe Lys Cys Met Glu Cys Glu Lys			
Ala Phe Ser Cys Ser Ser Asn Tyr Ile Val His Gln Arg Ile His	530	535	540
Thr Gly Glu Lys Pro Phe Gln Cys Lys Glu Cys Gly Lys Ala Phe	545	550	555
His Val Asn Ala His Leu Ile Arg His Gln Arg Ser His Thr Gly	560	565	570
Glu Lys Pro Phe Arg Cys Val Glu Cys Gly Lys Gly Phe Ser Phe	575	580	585
Ser Ser Asp Tyr Ile Ile His Gln Thr Val His Thr Trp Lys Lys	590	595	600
Pro Tyr Met Cys Ser Val Cys Gly Lys Ala Phe Arg Phe Ser Phe	605	610	615
Gln Leu Ser Gln His Gln Ser Val His Ser Glu Gly Lys Ser	620	625	630
	635	640	

<210> 77

<211> 194

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3094001CD1

<400> 77

Met Pro Ser Ser Pro Leu Arg Val Ala Val Val Cys Ser Ser Asn			
1 5 10 15			
Gln Asn Arg Ser Met Glu Ala His Asn Ile Leu Ser Lys Arg Gly	20	25	30
Phe Ser Val Arg Ser Phe Gly Thr Gly Thr His Val Lys Leu Pro	35	40	45
Gly Pro Ala Pro Asp Lys Pro Asn Val Tyr Asp Phe Lys Thr Thr	50	55	60
Tyr Asp Gln Met Tyr Asn Asp Leu Leu Arg Lys Asp Lys Glu Leu	65	70	75
Tyr Thr Gln Asn Gly Ile Leu His Met Leu Asp Arg Asn Lys Arg	80	85	90
Ile Lys Pro Arg Pro Glu Arg Phe Gln Asn Cys Lys Asp Leu Phe	95	100	105
Asp Leu Ile Leu Thr Cys Glu Glu Arg Val Tyr Asp Gln Val Val	110	115	120
Glu Asp Leu Asn Ser Arg Glu Gln Glu Thr Cys Gln Pro Val His	125	130	135
Val Val Asn Val Asp Ile Gln Asp Asn His Glu Glu Ala Thr Leu	140	145	150
Gly Ala Phe Leu Ile Cys Glu Leu Cys Gln Cys Ile Gln His Thr	155	160	165
Glu Asp Met Glu Asn Glu Ile Asp Glu Leu Leu Gln Glu Phe Glu	170	175	180
Glu Lys Ser Gly Arg Thr Phe Leu His Thr Val Cys Phe Tyr	185	190	

<210> 78

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3110061CD1

<400> 78

Met	Ala	Glu	Met	Asp	Pro	Thr	Gln	Gly	Arg	Val	Val	Phe	Glu	Asp
1				5					10					15
Val	Ala	Ile	Tyr	Phe	Ser	Gln	Glu	Glu	Trp	Gly	His	Leu	Asp	Glu
				20					25					30
Ala	Gln	Arg	Leu	Leu	Tyr	Arg	Asp	Val	Met	Leu	Glu	Asn	Leu	Ala
				35					40					45
Leu	Leu	Ser	Ser	Leu	Gly	Ser	Trp	His	Gly	Ala	Glu	Asp	Glu	Glu
				50					55					60
Ala	Pro	Ser	Gln	Gln	Gly	Phe	Ser	Val	Gly	Val	Ser	Glu	Val	Thr
				65					70					75
Thr	Ser	Lys	Pro	Cys	Leu	Ser	Ser	Gln	Lys	Val	His	Pro	Ser	Glu
				80					85					90
Thr	Cys	Gly	Pro	Pro	Leu	Lys	Asp	Ile	Leu	Cys	Leu	Val	Glu	His
				95					100					105
Asn	Gly	Ile	His	Pro	Glu	Gln	His	Ile	Tyr	Ile	Cys	Glu	Ala	Glu
				110					115					120
Leu	Phe	Gln	His	Pro	Lys	Gln	Gln	Ile	Gly	Glu	Asn	Leu	Ser	Arg
				125					130					135
Gly	Asp	Asp	Trp	Ile	Pro	Ser	Phe	Gly	Lys	Asn	His	Arg	Val	His
				140					145					150
Met	Ala	Glu	Glu	Ile	Phe	Thr	Cys	Met	Glu	Gly	Trp	Lys	Asp	Leu
				155					160					165
Pro	Ala	Thr	Ser	Cys	Leu	Leu	Gln	His	Gln	Gly	Pro	Gln	Ser	Glu
				170					175					180
Trp	Lys	Pro	Tyr	Arg	Asp	Thr	Glu	Asp	Arg	Glu	Ala	Phe	Gln	Thr
				185					190					195
Gly	Gln	Asn	Asp	Tyr	Lys	Cys	Ser	Glu	Cys	Gly	Lys	Thr	Phe	Thr
				200					205					210
Cys	Ser	Tyr	Ser	Phe	Val	Glu	His	Gln	Lys	Ile	His	Thr	Gly	Glu
				215					220					225
Arg	Ser	Tyr	Glu	Cys	Asn	Lys	Cys	Gly	Lys	Phe	Phe	Lys	Tyr	Ser
				230					235					240
Ala	Asn	Phe	Met	Lys	His	Gln	Thr	Val	His	Thr	Ser	Glu	Arg	Thr
				245					250					255
Tyr	Glu	Cys	Arg	Glu	Cys	Gly	Lys	Ser	Phe	Met	Tyr	Asn	Tyr	Arg
				260					265					270
Leu	Met	Arg	His	Lys	Arg	Val	His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu
				275					280					285
Cys	Asn	Thr	Cys	Gly	Lys	Phe	Phe	Arg	Tyr	Ser	Ser	Thr	Phe	Val
				290					295					300
Arg	His	Gln	Arg	Phe	His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Arg
				305					310					315
Glu	Cys	Gly	Lys	Phe	Phe	Met	Asp	Ser	Ser	Thr	Leu	Ile	Lys	His
				320					325					330
Gln	Arg	Val	His	Thr	Gly	Glu	Arg	Pro	Tyr	Lys	Cys	Asn	Asp	Cys
				335					340					345
Gly	Lys	Phe	Phe	Arg	Tyr	Ile	Ser	Thr	Leu	Ile	Arg	His	Gln	Arg
				350					355					360
Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Ser	Val	Cys	Gly	Glu
				365					370					375
Leu	Phe	Arg	Tyr	Asn	Ser	Ser	Leu	Val	Lys	His	Trp	Arg	Asn	His
				380					385					390
Thr	Gly	Glu	Arg	Pro	Tyr	Lys	Cys	Ser	Glu	Cys	Gly	Lys	Ser	Phe
				395					400					405
Arg	Tyr	His	Cys	Arg	Leu	Ile	Arg	His	Gln	Arg	Val	His	Thr	Gly
				410					415					420
Glu	Arg	Pro	Tyr	Glu	Cys	Ser	Glu	Cys	Gly	Lys	Phe	Phe	Arg	Tyr
				425					430					435
Asn	Ser	Asn	Leu	Ile	Lys	His	Trp	Arg	Asn	His	Thr	Gly	Glu	Arg
				440					445					450
Pro	Tyr	Glu	Cys	Arg	Glu	Cys	Gly	Lys	Ala	Phe	Ser	His	Lys	His
				455					460					465


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Ile Leu Val Glu His Gln Lys Ile His Ser Gly Glu Arg Pro Tyr
470 475 480
Glu Cys Ser Glu Cys Gln Lys Ala Phe Ile Arg Lys Ser His Leu
485 490 495
Val His His Gln Lys Ile His Ser Glu Glu Arg Leu Val Cys Ser
500 505 510
Met Asn Val Gly Asn Ser Leu Ala Lys Thr Pro Thr Ser Leu Asn
515 520 525
Ile Arg Asp Phe Thr Met Glu Lys Val Tyr His
530 535

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<210> 79
<211> 412
<212> PRT
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 3146614CD1

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<400> 79
Met Ser Phe Val Ala Tyr Glu Glu Leu Ile Lys Glu Gly Asp Thr
1 5 10 15
Ala Ile Leu Ser Leu Gly His Gly Ala Met Val Ala Val Arg Val
20 25 30
Gln Arg Gly Ala Gln Thr Gln Thr Arg His Gly Val Leu Arg His
35 40 45
Ser Val Asp Leu Ile Gly Arg Pro Phe Gly Ser Lys Val Thr Cys
50 55 60
Gly Arg Gly Gly Trp Val Tyr Val Leu His Pro Thr Pro Glu Leu
65 70 75
Trp Thr Leu Asn Leu Pro His Arg Thr Gln Ile Leu Tyr Ser Thr
80 85 90
Asp Ile Ala Leu Ile Thr Met Met Leu Glu Leu Arg Pro Gly Ser
95 100 105
Val Val Cys Glu Ser Gly Thr Gly Ser Gly Ser Val Ser His Ala
110 115 120
Ile Ile Arg Thr Ile Ala Pro Thr Gly His Leu His Thr Val Glu
125 130 135
Phe His Gln Gln Arg Ala Glu Lys Ala Arg Glu Glu Phe Gln Glu
140 145 150
His Arg Val Gly Arg Trp Val Thr Val Arg Thr Gln Asp Val Cys
155 160 165
Arg Ser Gly Phe Gly Val Ser His Val Ala Asp Ala Val Phe Leu
170 175 180
Asp Ile Pro Ser Pro Trp Glu Ala Val Gly His Ala Trp Asp Ala
185 190 195
Leu Lys Val Glu Gly Gly Arg Phe Cys Ser Phe Ser Pro Cys Ile
200 205 210
Glu Gln Val Gln Arg Thr Cys Gln Ala Leu Ala Ala Arg Arg Leu
215 220 225
Leu Arg Ala Glu His Pro Gly Gly Ala Ala Thr Gly Leu Gln Arg
230 235 240
Ala His Cys Gln Pro Ala Thr Ala Arg Pro Gly His Arg His Arg
245 250 255
Trp Pro Cys Arg Leu Arg His Gln Pro Leu Pro Gln Arg His Ala
260 265 270
His Glu Gly Gly Arg Gly Pro His Arg Leu Pro Asp Leu Arg His
275 280 285
Gln Asp Pro Arg Leu Gly Gly Arg Leu Pro Gly His Gln Gly Ala
290 295 300
Gly Ser Thr Glu Gly Leu Gly Arg Glu Ala Arg Gly Thr Leu Tyr
305 310 315

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Gly Gln Arg Cys Leu Pro Asp Thr Asp Gly Gly Val Gly Leu Gly
 320 325 330
 Gly Leu Leu Gly Gly Gln Ser Gly Thr Ala Gly Arg Ala Ala Val
 335 340 345
 Met Glu Glu Gln Cys Trp Gly Trp Ala Ser Ala Ile Pro Val Gln
 350 355 360
 Pro Cys Gly Pro Ser Gln Leu Leu Phe Val Ala Asn Met Lys Tyr
 365 370 375
 Pro Leu Pro Gln Ala Pro Leu Gly Val Glu Ala Lys Gly Cys Arg
 380 385 390
 Trp Gly Ser Leu Thr Pro Ser Gln Val Gly Leu Ser Arg Lys Gly
 395 400 405
 Val Glu Glu Gly Gly Gly His
 410

<210> 80

<211> 482

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3295381CD1

<400> 80

Met Ala Lys Leu Tyr Glu Ala Val Thr Phe Lys Asp Val Ala Val
 1 5 10 15
 Ile Phe Thr Glu Glu Glu Leu Gly Leu Leu Asp Pro Ala Gln Arg
 20 25 30
 Lys Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Arg Asn Leu Leu
 35 40 45
 Ser Val Gly His Gln Pro Phe His Gly Asp Thr Phe His Phe Leu
 50 55 60
 Arg Glu Glu Lys Phe Trp Val Met Gly Thr Thr Ser Gln Arg Glu
 65 70 75
 Gly Asn Leu Gly Gly Glu Ile Gln Thr Glu Met Glu Thr Val Pro
 80 85 90
 Glu Ala Gly Thr His Glu Glu Phe Ser Cys Lys Gln Ile Trp Glu
 95 100 105
 Gln Ile Ala Ser Asp Leu Thr Gly Ser Gln Asp Thr Thr Ile Ser
 110 115 120
 Asn Ser Gln Leu Phe Glu Gln Asp Asp Asn Pro Ser Gln Ile Lys
 125 130 135
 Ala Arg Leu Ser Thr Val His Thr Arg Glu Lys Pro Phe Gln Gly
 140 145 150
 Glu Asn Cys Lys Gln Phe Phe Ser Asp Val Ser Phe Phe Asp Leu
 155 160 165
 Pro Gln Gln Leu Tyr Ser Gly Glu Lys Ser His Thr Cys Asp Glu
 170 175 180
 Cys Gly Lys Ser Phe Cys Tyr Ile Ser Ala Leu His Ile His Gln
 185 190 195
 Arg Val His Met Gly Val Lys Cys Tyr Lys Cys Asp Val Cys Gly
 200 205 210
 Lys Glu Phe Ser Gln Ser Ser Arg Leu Gln Thr His Gln Arg Val
 215 220 225
 His Thr Gly Glu Lys Pro Phe Lys Cys Glu Gln Cys Gly Lys Gly
 230 235 240
 Phe Arg Cys Arg Ser Ala Leu Lys Val His Cys Lys Leu His Met
 245 250 255
 Arg Glu Lys Pro Tyr Asn Cys Glu Lys Cys Gly Lys Ala Phe Met
 260 265 270
 His Asn Phe Gln Leu Gln Lys His His Arg Ile His Thr Gly Glu
 275 280 285

Lys Pro Phe Lys Cys Glu Ile Cys Gly Lys Ser Phe Cys Leu Arg
 290 300
 Ser Ser Leu Asn Arg His Cys Met Val His Thr Ala Glu Lys Leu
 305 315
 Tyr Lys Ser Glu Lys Tyr Gly Arg Gly Phe Ile Asp Arg Leu Asp
 320 330
 Leu His Lys His Gln Met Ile His Met Gly Gln Lys Pro Tyr Asn
 335 345
 Cys Lys Glu Cys Gly Lys Ser Phe Lys Trp Ser Ser Tyr Leu Leu
 350 360
 Val His Gln Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys Glu
 365 375
 Glu Cys Gly Lys Gly Tyr Ile Ser Lys Ser Gly Leu Asp Phe His
 380 390
 His Arg Thr His Thr Gly Glu Arg Ser Tyr Asn Cys Asp Asn Cys
 395 405
 Gly Lys Ser Phe Arg His Ala Ser Ser Ile Leu Asn His Lys Lys
 410 420
 Leu His Cys Gln Arg Lys Pro Leu Lys Cys Glu Asp Cys Gly Lys
 425 435
 Arg Leu Val Cys Arg Ser Tyr Cys Lys Asp Gln Gln Arg Asp His
 440 450
 Ser Gly Glu Asn Pro Ser Lys Cys Glu Asp Cys Gly Lys Arg Tyr
 455 465
 Lys Arg Arg Leu Asn Leu Asp Ile Ile Leu Ser Leu Phe Leu Asn
 470 480
 Asp Ile

<210> 81

<211> 554

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3364774CD1

<400> 81

Met Ser Ala Asp Gly Gly Gly Ile Gln Asp Thr Gln Asp Lys Glu
 1 5 10 15
 Thr Pro Pro Glu Val Pro Asp Arg Gly His Pro His Gln Glu Met
 20 25 30
 Pro Ser Lys Leu Gly Glu Ala Val Pro Ser Gly Asp Thr Gln Glu
 35 40 45
 Ser Leu His Ile Lys Met Glu Pro Glu Glu Pro His Ser Glu Gly
 50 55 60
 Ala Ser Gln Glu Asp Gly Ala Gln Gly Ala Trp Gly Trp Ala Pro
 65 70 75
 Leu Ser His Gly Ser Lys Glu Lys Ala Leu Phe Leu Pro Gly Gly
 80 85 90
 Ala Leu Pro Ser Pro Arg Ile Pro Val Leu Ser Arg Glu Gly Arg
 95 100 105
 Thr Arg Asp Arg Gln Met Ala Ala Ala Leu Thr Ala Trp Ser
 110 115 120
 Gln Met Pro Val Thr Phe Glu Asp Val Ala Leu Tyr Leu Ser Arg
 125 130 135
 Glu Glu Trp Gly Arg Leu Asp His Thr Gln Gln Asn Phe Tyr Arg
 140 145 150
 Asp Val Leu Gln Lys Lys Asn Gly Leu Ser Leu Gly Phe Pro Phe
 155 160 165
 Ser Arg Pro Phe Trp Ala Pro Gln Ala His Gly Lys Gly Glu Ala
 170 175 180

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Ser Gly Ser Ser Arg Gln Ala Gly Asp Glu Lys Glu Trp Arg Gly
185 190 195
Ala Cys Thr Gly Ala Val Glu Val Gly Gln Arg Val Gln Thr Ser
200 205 210
Ser Val Ala Ala Leu Gly Asn Val Lys Pro Phe Arg Thr Arg Ala
215 220 225
Gly Arg Val Gln Trp Gly Val Pro Gln Cys Ala Gln Glu Ala Ala
230 235 240
Cys Gly Arg Ser Ser Gly Pro Ala Lys Asp Ser Gly Gln Pro Ala
245 250 255
Glu Pro Asp Arg Thr Pro Asp Ala Ala Pro Pro Asp Pro Ser Pro
260 265 270
Thr Glu Pro Gln Glu Tyr Arg Val Pro Glu Lys Pro Asn Glu Glu
275 280 285
Glu Lys Gly Ala Pro Glu Ser Gly Glu Glu Gly Leu Ala Pro Asp
290 295 300
Ser Glu Val Gly Arg Lys Ser Tyr Arg Cys Glu Gln Cys Gly Lys
305 310 315
Gly Phe Ser Trp His Ser His Leu Val Thr His Arg Arg Thr His
320 325 330
Thr Gly Glu Lys Pro Tyr Ala Cys Thr Asp Cys Gly Lys Arg Phe
335 340 345
Gly Arg Ser Ser His Leu Ile Gln His Gln Ile Ile His Thr Gly
350 355 360
Glu Lys Pro Tyr Thr Cys Pro Ala Cys Arg Lys Ser Phe Ser His
365 370 375
His Ser Thr Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys
380 385 390
Pro Tyr Val Cys Asp Arg Cys Ala Lys Arg Phe Thr Arg Arg Ser
395 400 405
Asp Leu Val Thr His Gln Gly Thr His Thr Gly Ala Lys Pro His
410 415 420
Lys Cys Pro Ile Cys Ala Lys Cys Phe Thr Gln Ser Ser Ala Leu
425 430 435
Val Thr His Gln Arg Thr His Thr Gly Val Lys Pro Tyr Pro Cys
440 445 450
Pro Glu Cys Gly Lys Cys Phe Ser Gln Arg Ser Asn Leu Ile Ala
455 460 465
His Asn Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Leu Asp
470 475 480
Cys Gly Lys Ser Phe Ser His Ser Ser His Leu Thr Ala His Gln
485 490 495
Arg Thr His Arg Gly Val Arg Pro Tyr Ala Cys Pro Leu Cys Gly
500 505 510
Lys Ser Phe Ser Arg Arg Ser Asn Leu His Arg His Glu Lys Ile
515 520 525
His Thr Thr Gly Pro Lys Ala Leu Ala Met Leu Met Leu Gly Ala
530 535 540
Ala Ala Ala Gly Ala Leu Ala Thr Pro Pro Pro Ala Pro Thr
545 550

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<210> 82

<211> 488

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3397777CD1

<400> 82

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Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys
1 5 10 15

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Pro	Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	
				20					25					30	
Gly	His	Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	
				35					40					45	
Ala	Val	Thr	Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	
				50					55					60	
Ile	Ser	Tyr	Ser	Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	
				65					70					75	
Asn	Ile	Val	Glu	Arg	Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	
				80					85					90	
Gly	Lys	Lys	Arg	Asp	Leu	Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	
				95					100					105	
Leu	Phe	Cys	Lys	Glu	Asp	Arg	Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	
				110					115					120	
Arg	Ser	Gln	Glu	His	Arg	Gly	His	His	Thr	Val	Leu	Thr	Glu	Glu	
				125					130					135	
Val	Phe	Lys	Glu	Cys	Gln	Glu	Glu	Leu	Gln	Ala	Val	Leu	Lys	Arg	
				140					145					150	
Leu	Lys	Thr	Glu	Glu	Glu	Glu	Ala	Glu	Lys	Leu	Glu	Ala	Asp	Ile	
				155					160					165	
Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val	Gln	Thr	Glu	Arg	
				170					175					180	
Gln	Arg	Leu	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser	Ile	Leu	Asn	
				185					190					195	
Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Lys	Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val	Gln	
				215					220					225	
Gln	Lys	Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg	
				230					235					240	
Ser	Gln	Trp	Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	
				245					250					255	
Met	Lys	Trp	Ser	Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	
				260					265					270	
Ser	Lys	Lys	Leu	Lys	Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	
				275					280					285	
Met	Leu	Gln	Met	Phe	Arg	Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	
				290					295					300	
Val	Asp	Val	Thr	Leu	Asn	Ser	Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	
				305					310					315	
Leu	Ser	Glu	Asp	Gln	Arg	Gln	Val	Ile	Ser	Val	Pro	Ile	Trp	Pro	
				320					325					330	
Phe	Gln	Trp	Tyr	Asn	Tyr	Gly	Val	Leu	Gly	Ser	Gln	Tyr	Phe	Ser	
				335					340					345	
Ser	Gly	Lys	His	Tyr	Trp	Glu	Val	Asp	Val	Ser	Lys	Lys	Thr	Ala	
				350					355					360	
Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg	Thr	Tyr	Ser	Arg	His	Met	Lys	
				365					370					375	
Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg	Gln	Asn	Leu	Tyr	Thr	Lys	
				380					385					390	
Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile	Gly	Leu	Gln	Asn	Lys	
				395					400					405	
Cys	Lys	Tyr	Gly	Val	Phe	Glu	Glu	Ser	Leu	Ser	Ser	Asp	Pro	Glu	
				410					415					420	
Val	Leu	Thr	Leu	Ser	Met	Ala	Val	Pro	Pro	Cys	Arg	Val	Gly	Val	
				425					430					435	
Phe	Leu	Asp	Tyr	Glu	Ala	Gly	Ile	Val	Ser	Phe	Phe	Asn	Val	Thr	
				440					445					450	
Ser	His	Gly	Ser	Leu	Ile	Tyr	Lys	Phe	Ser	Lys	Cys	Cys	Phe	Ser	
				455					460					465	
Gln	Pro	Val	Tyr	Pro	Tyr	Phe	Asn	Pro	Trp	Asn	Cys	Pro	Ala	Pro	
				470					475					480	
Met	Thr	Leu	Cys	Pro	Pro	Ser	Ser								

485

<210> 83
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3403046CD1

<400> 83
 Met Ser Gln Gly Leu Pro Ala Ala Gly Ser Ile Leu Gln Arg Ser
 1 5 10 15
 Val Ala Ala Pro Gly Asn Gln Pro Gln Pro Gln Pro Gln Gln Gln
 20 25 30
 Ser Pro Glu Asp Asp Asp Arg Lys Val Arg Arg Arg Glu Lys Asn
 35 40 45
 Arg Val Ala Ala Gln Arg Ser Arg Lys Lys Gln Thr Gln Lys Ala
 50 55 60
 Asp Lys Leu His Glu Glu Tyr Glu Ser Leu Glu Gln Glu Asn Thr
 65 70 75
 Met Leu Arg Arg Glu Ile Gly Lys Leu Thr Glu Glu Leu Lys His
 80 85 90
 Leu Thr Glu Ala Leu Lys Glu His Glu Lys Met Cys Pro Leu Leu
 95 100 105
 Leu Cys Pro Met Asn Phe Val Pro Val Pro Pro Arg Pro Asp Pro
 110 115 120
 Val Ala Gly Cys Leu Pro Arg
 125

<210> 84
 <211> 532
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3538506CD1

<400> 84
 Met Arg Cys Asp Phe Cys Gly Ala Gly Phe Asp Thr Arg Ala Gly
 1 5 10 15
 Leu Ser Ser His Ala Arg Ala His Leu Arg Asp Phe Gly Ile Thr
 20 25 30
 Asn Trp Glu Leu Thr Val Ser Pro Ile Asn Ile Leu Gln Glu Leu
 35 40 45
 Leu Ala Thr Ser Ala Ala Glu Gln Pro Pro Ser Pro Leu Gly Arg
 50 55 60
 Glu Pro Gly Gly Pro Pro Gly Ser Phe Leu Thr Ser Arg Arg Pro
 65 70 75
 Arg Leu Pro Leu Thr Val Pro Phe Pro Pro Thr Trp Ala Glu Asp
 80 85 90
 Pro Gly Pro Ala Tyr Gly Asp Ala Ser Gly Pro Glu Pro Ala Arg
 95 100 105
 Asp Ile Arg Cys Glu Phe Cys Gly Glu Phe Phe Glu Asn Arg Lys
 110 115 120
 Gly Leu Ser Ser His Ala Arg Ser His Leu Arg Gln Met Gly Val
 125 130 135
 Thr Glu Trp Tyr Val Asn Gly Ser Pro Ile Asp Thr Leu Arg Glu
 140 145 150
 Ile Leu Lys Arg Arg Thr Gln Ser Arg Pro Gly Gly Pro Pro Asn
 155 160 165

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Pro Pro Gly Pro Ser Pro Lys Ala Leu Ala Lys Met Met Gly Gly
170 175 180
Ala Gly Pro Gly Ser Ser Leu Glu Ala Arg Ser Pro Ser Asp Leu
185 190 195
His Ile Ser Pro Leu Ala Lys Lys Leu Pro Pro Pro Pro Gly Ser
200 205 210
Pro Leu Gly His Ser Pro Thr Ala Ser Pro Pro Pro Thr Ala Arg
215 220 225
Lys Met Phe Pro Gly Leu Ala Ala Pro Ser Leu Pro Lys Lys Leu
230 235 240
Lys Pro Glu Gln Ile Arg Val Glu Ile Lys Arg Glu Met Leu Pro
245 250 255
Gly Ala Leu His Gly Glu Leu His Pro Ser Glu Gly Pro Trp Gly
260 265 270
Ala Pro Arg Glu Asp Met Thr Pro Leu Asn Leu Ser Ser Arg Ala
275 280 285
Glu Pro Val Arg Asp Ile Arg Cys Glu Phe Cys Gly Glu Phe Phe
290 295 300
Glu Asn Arg Lys Gly Leu Ser Ser His Ala Arg Ser His Leu Arg
305 310 315
Gln Met Gly Val Thr Glu Trp Ser Val Asn Gly Ser Pro Ile Asp
320 325 330
Thr Leu Arg Glu Ile Leu Lys Lys Lys Ser Lys Pro Cys Leu Ile
335 340 345
Lys Lys Glu Pro Pro Ala Gly Asp Leu Ala Pro Ala Leu Ala Glu
350 355 360
Asp Gly Pro Pro Thr Val Ala Pro Gly Pro Val Gln Ser Pro Leu
365 370 375
Pro Leu Ser Pro Leu Ala Gly Arg Pro Gly Lys Pro Gly Ala Gly
380 385 390
Pro Ala Gln Val Pro Arg Glu Leu Ser Leu Thr Pro Ile Thr Gly
395 400 405
Ala Lys Pro Ser Ala Thr Gly Tyr Leu Gly Ser Val Ala Ala Lys
410 415 420
Arg Pro Leu Gln Glu Asp Arg Leu Leu Pro Ala Glu Val Lys Ala
425 430 435
Lys Thr Tyr Ile Gln Thr Glu Leu Pro Phe Lys Ala Lys Thr Leu
440 445 450
His Glu Lys Thr Ser His Ser Ser Thr Glu Ala Cys Cys Glu Leu
455 460 465
Cys Gly Leu Tyr Phe Glu Asn Arg Lys Ala Leu Ala Ser His Ala
470 475 480
Arg Ala His Leu Arg Gln Phe Gly Val Thr Glu Trp Cys Val Asn
485 490 495
Gly Ser Pro Ile Glu Thr Leu Ser Glu Trp Ile Lys His Arg Pro
500 505 510
Gln Lys Val Gly Ala Tyr Arg Ser Tyr Ile Gln Gly Gly Arg Lys
515 520 525
Leu Ile Pro Phe Ser Glu Gly
530

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<210> 85

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3575519CD1

<400> 85

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Met Asp Tyr Lys Ser Ser Leu Ile Gln Asp Gly Asn Pro Met Glu
1 5 10 15

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Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met Phe
    20                25                30
Thr Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
    35                40                45
Lys Cys Ala Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr
    50                55                60
Ser Arg Gly Ser Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys
    65                70                75
Pro Thr Cys Arg His Glu Val Ile Met Asp Arg His Gly Val Tyr
    80                85                90
Gly Leu Gln Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr
    95                100               105
Lys Gln Glu Cys Ser Ser Arg Pro Leu Gln Lys Gly Ser His Pro
   110               115               120
Met Cys Lys Glu His Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu
   125               130               135
Thr Cys Glu Val Pro Thr Cys Ser Met Cys Lys Val Phe Gly Ile
   140               145               150
His Lys Ala Cys Glu Val Ala Pro Leu Gln Ser Val Phe Gln Gly
   155               160               165
Gln Lys Thr Glu Leu Asn Asn Cys Ile Ser Met Leu Val Ala Gly
   170               175               180
Asn Asp Arg Val Gln Thr Ile Ile Thr Gln Leu Glu Asp Ser Arg
   185               190               195
Arg Val Thr Lys Glu Asn Ser His Gln Val Lys Glu Glu Leu Ser
   200               205               210
Gln Lys Phe Asp Thr Leu Tyr Ala Ile Leu Asp Glu Lys Lys Ser
   215               220               225
Glu Leu Leu Gln Arg Ile Thr Gln Glu Gln Glu Lys Lys Leu Ser
   230               235               240
Phe Ile Glu Ala Leu Ile Gln Gln Tyr Gln Glu Gln Leu Asp Lys
   245               250               255
Ser Thr Lys Leu Val Glu Thr Ala Ile Gln Ser Leu Asp Glu Pro
   260               265               270
Gly Gly Ala Thr Phe Leu Leu Thr Ala Lys Gln Leu Ile Lys Ser
   275               280               285
Ile Val Glu Ala Ser Lys Gly Cys Gln Leu Gly Lys Thr Glu Gln
   290               295               300
Gly Phe Glu Asn Met Asp Phe Phe Thr Leu Asp Leu Glu His Ile
   305               310               315
Ala Asp Ala Leu Arg Ala Ile Asp Phe Gly Thr Asp Glu Glu Glu
   320               325               330
Glu Glu Phe Ile Glu Glu Glu Asp Gln Glu Glu Glu Glu Ser Thr
   335               340               345
Glu Gly Lys Glu Glu Gly His Gln
   350

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<210> 86

<211> 407

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3598694CD1

<400> 86

```

Met Leu Ser Gln Ile Met Glu Asn Pro Leu Val Gln Asp Met Met
  1      5      10
Ser Asn Pro Asp Leu Met Arg His Met Ile Met Ala Asn Pro Gln
  20      25      30
Met Gln Gln Leu Met Glu Arg Asn Pro Glu Ile Ser His Met Leu
  35      40      45

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Asn Asn Pro Glu Leu Met Arg Gln Thr Met Glu Leu Ala Arg Asn
50 55 60
Pro Ala Met Met Gln Glu Met Met Arg Asn Gln Asp Arg Ala Leu
65 70 75
Ser Asn Leu Glu Ser Ile Pro Gly Gly Tyr Asn Ala Leu Arg Arg
80 85 90
Met Tyr Thr Asp Ile Gln Glu Pro Met Phe Ser Ala Ala Arg Glu
95 100 105
Gln Phe Gly Asn Asn Pro Phe Ser Ser Leu Ala Gly Asn Ser Asp
110 115 120
Ser Ser Ser Ser Gln Pro Leu Arg Thr Glu Asn Arg Glu Pro Leu
125 130 135
Pro Asn Pro Trp Ser Pro Ser Pro Pro Thr Ser Gln Ala Pro Gly
140 145 150
Ser Gly Gly Glu Gly Thr Gly Gly Ser Gly Thr Ser Gln Val His
155 160 165
Pro Thr Val Ser Asn Pro Phe Gly Ile Asn Ala Ala Ser Leu Gly
170 175 180
Ser Gly Met Phe Asn Ser Pro Glu Met Gln Ala Leu Leu Gln Gln
185 190 195
Ile Ser Glu Asn Pro Gln Leu Met Gln Asn Val Ile Ser Ala Pro
200 205 210
Tyr Met Arg Ser Met Met Gln Thr Leu Ala Gln Asn Pro Asp Phe
215 220 225
Ala Ala Gln Met Met Val Asn Val Pro Leu Phe Ala Gly Asn Pro
230 235 240
Gln Leu Gln Glu Gln Leu Arg Leu Gln Leu Pro Val Phe Leu Gln
245 250 255
Gln Met Gln Asn Pro Glu Ser Leu Ser Ile Leu Thr Asn Pro Arg
260 265 270
Ala Met Gln Ala Leu Leu Gln Ile Gln Gln Gly Leu Gln Thr Leu
275 280 285
Gln Thr Glu Ala Pro Gly Leu Val Pro Ser Leu Gly Ser Phe Gly
290 295 300
Met Ser Arg Thr Pro Ala Pro Ser Ala Gly Ser Asn Ala Gly Ser
305 310 315
Thr Pro Glu Ala Pro Thr Ser Ser Pro Ala Thr Pro Ala Thr Ser
320 325 330
Ser Pro Thr Gly Ala Ser Ser Ala Gln Gln Gln Leu Met Gln Gln
335 340 345
Met Ile Gln Leu Leu Ala Gly Ser Gly Asn Ser Gln Val Gln Thr
350 355 360
Pro Glu Val Arg Phe Gln Gln Gln Leu Glu Gln Leu Asn Ser Met
365 370 375
Gly Phe Ile Asn Arg Glu Ala Asn Leu Gln Ala Leu Ile Ala Thr
380 385 390
Gly Gly Asp Ile Asn Ala Ala Ile Glu Arg Leu Leu Gly Ser Gln
395 400 405
Leu Ser

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<210> 87

<211> 350

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3638819CD1

<220>

<221> unsure

<222> 301

<223> unknown or other

<400> 87

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Met Leu Leu Asn Pro Glu Glu Lys Ser Pro Leu Asn Ile Ser Val
  1          5          10          15
Gly Val His Pro Leu Asp Ser Phe Thr Gln Gly Phe Gly Glu Gln
          20          25          30
Pro Thr Gly Asp Leu Pro Ile Gly Pro Pro Phe Glu Met Pro Thr
          35          40          45
Gly Ala Leu Leu Ser Thr Pro Gln Phe Glu Met Leu Gln Asn Pro
          50          55          60
Leu Gly Leu Thr Gly Ala Leu Arg Gly Pro Gly Arg Arg Gly Gly
          65          70          75
Arg Ala Arg Gly Gly Gln Gly Pro Arg Pro Asn Ile Cys Gly Ile
          80          85          90
Cys Gly Lys Ser Phe Gly Arg Gly Ser Thr Pro Ile Gln His Gln
          95          100          105
Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Val Cys Ser
          110          115          120
Lys Ala Phe Ser Gln Ser Ser Asp Leu Ile Lys His Gln Arg Thr
          125          130          135
His Thr Gly Glu Arg Pro Tyr Lys Cys Pro Arg Cys Gly Lys Ala
          140          145          150
Phe Ala Asp Ser Ser Tyr Leu Leu Arg His Gln Arg Thr His Ser
          155          160          165
Gly Gln Lys Pro Phe Lys Cys Pro His Cys Gly Lys Ala Phe Gly
          170          175          180
Asp Ser Ser Tyr Leu Leu Arg His Gln Arg Thr His Ser His Glu
          185          190          195
Arg Pro Tyr Ser Cys Thr Glu Cys Gly Lys Cys Tyr Ser Gln Asn
          200          205          210
Ser Ser Leu Arg Ser His Gln Arg Val His Thr Gly Gln Arg Pro
          215          220          225
Phe Ser Cys Gly Ile Cys Gly Lys Ser Phe Ser Gln Arg Ser Ala
          230          235          240
Leu Ile Pro His Ala Arg Ser His Ala Arg Glu Lys Pro Phe Lys
          245          250          255
Cys Leu Ser Cys Ala Asn Val Leu Ala Glu Leu Gly Ala Gly Asn
          260          265          270
Pro Arg Pro His Pro Leu Gly Gly Gly Arg Gly Trp Gly Gly Leu
          275          280          285
Cys Gly Gly Val Val Gly Trp Gly Gly Cys Gly Gly Glu Trp Gly
          290          295          300
Xaa Val Gly His Gly Val Gly Gly Val Leu Gly Val Val Gly Val
          305          310          315
Phe Cys Phe Phe Phe Ala Phe Trp Leu Phe Cys Phe Tyr Pro Phe
          320          325          330
Arg Trp Leu Phe Phe Pro Arg Asn Pro Phe Gly Ser Leu Ser Phe
          335          340          345
Trp Phe Pro Pro Val
          350

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<210> 88

<211> 215

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3717139CD1

<400> 88

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Met His Val Trp Pro Arg Trp Val Pro Pro Pro Val Ser Pro Glu

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1	5	10	15
Leu Lys Asp Arg	Lys Glu Asp Ala Lys	Gly Met Glu Asp Glu	Gly
	20	25	30
Gln Thr Lys Ile	Lys Gln Arg Arg Ser	Arg Thr Asn Phe Thr	Leu
	35	40	45
Glu Gln Leu Asn	Glu Leu Glu Arg Leu	Phe Asp Glu Thr His	Tyr
	50	55	60
Pro Asp Ala Phe	Met Arg Glu Glu Leu	Ser Gln Arg Leu Gly	Leu
	65	70	75
Ser Glu Ala Arg	Val Gln Val Trp Phe	Gln Asn Arg Arg Ala	Lys
	80	85	90
Cys Arg Lys Gln	Glu Asn Gln Leu His	Lys Gly Val Leu Ile	Gly
	95	100	105
Ala Ala Ser Gln	Phe Glu Ala Cys Arg	Val Ala Pro Tyr Val	Asn
	110	115	120
Val Gly Ala Leu	Arg Met Pro Phe Gln	Gln Val Gln Ala Gln	Leu
	125	130	135
Gln Leu Asp Ser	Ala Val Ala His Ala	His His Leu His	Pro
	140	145	150
His Leu Ala Ala	His Ala Pro Tyr Met	Met Phe Pro Ala Pro	Pro
	155	160	165
Phe Gly Leu Pro	Leu Ala Thr Leu Ala	Ala Asp Ser Ala Ser	Ala
	170	175	180
Ala Ser Val Val	Ala Ala Ala Ala Ala	Lys Thr Thr Ser	Lys
	185	190	195
Asn Ser Ser Ile	Ala Asp Leu Arg Leu	Lys Ala Lys Lys His	Ala
	200	205	210
Ala Ala Leu Gly	Leu		
	215		

<210> 89

<211> 489

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3892962CD1

<400> 89

Met Lys Glu Leu Asp	Pro Lys Asn Asp Ile	Ser Glu Asp Lys Leu
1	5	10
Ser Val Val Gly	Glu Ala Thr Gly Gly	Pro Thr Arg Asn Gly Ala
	20	25
Arg Gly Pro Gly	Ser Glu Gly Val Trp	Glu Pro Gly Ser Trp Pro
	35	40
Glu Arg Pro Arg	Gly Asp Ala Gly Ala	Glu Trp Glu Pro Leu Gly
	50	55
Ile Pro Gln Gly	Asn Lys Leu Leu Gly	Ser Val Pro Ala Cys
	65	70
His Glu Leu Lys	Ala Phe Ala Asn Gln	Gly Cys Val Leu Val Pro
	80	85
Pro Arg Leu Asp	Asp Pro Thr Glu Lys	Gly Ala Cys Pro Pro Val
	95	100
Arg Arg Gly Lys	Asn Phe Ser Ser Thr	Ser Asp Leu Ser Lys Pro
	110	115
Pro Met Pro Cys	Glu Glu Lys Lys Thr	Tyr Asp Cys Ser Glu Cys
	125	130
Gly Lys Ala Phe	Ser Arg Ser Ser Ser	Leu Ile Lys His Gln Arg
	140	145
Ile His Thr Gly	Glu Lys Pro Phe Glu	Cys Asp Thr Cys Gly Lys
	155	160
His Phe Ile Glu	Arg Ser Ser Leu Thr	Ile His Gln Arg Val His

Thr Gly Glu Lys	170	Pro Tyr Ala Cys Gly	175	Asp Cys Gly Lys Ala Phe	180
	185		190		195
Ser Gln Arg Met	200	Asn Leu Thr Val His	205	Gln Arg Thr His Thr Gly	210
	215		220		225
Glu Lys Pro Tyr	230	Val Cys Asp Val Cys	235	Gly Lys Ala Phe Arg Lys	240
	245		250		255
Thr Ser Ser Leu	260	Gln His Glu Arg	265	Ile His Thr Gly Glu Lys	270
	275		280		285
Pro Tyr Ala Cys	290	Gly Asp Cys Gly Lys	295	Ala Phe Ser Gln Asn Met	300
	305		310		315
His Leu Ile Val	320	His Gln Arg Thr His	325	Thr Gly Glu Lys Pro Tyr	330
	335		340		345
Val Cys Pro Glu	350	Cys Gly Arg Ala Phe	355	Ser Gln Asn Met His Leu	360
	365		370		375
Thr Glu His Gln	380	Arg Thr His Thr Gly	385	Glu Lys Pro Tyr Ala Cys	390
	395		400		405
Lys Glu Cys Gly	410	Lys Ala Phe Asn Lys	415	Ser Ser Ser Leu Thr Leu	420
	425		430		435
His Gln Arg Asn	440	His Thr Gly Glu Lys	445	Pro Tyr Val Cys Gly Glu	450
	455		460		465
Cys Gly Lys Ala	470	Phe Ser Gln Ser Ser	475	Tyr Leu Ile Gln His Gln	480
	485				
Arg Phe His Ile		Gly Val Lys Pro Phe		Glu Cys Ser Glu Cys Gly	
Lys Ala Phe Ser		Lys Asn Ser Ser Leu		Thr Gln His Gln Arg Ile	
His Thr Gly Glu		Lys Pro Tyr Glu Cys		Tyr Ile Cys Lys Lys His	
Phe Thr Gly Arg		Ser Ser Leu Ile Val		His Gln Ile Val His Thr	
Gly Glu Lys Pro		Tyr Val Cys Gly Glu		Cys Gly Lys Ala Phe Ser	
Gln Ser Ala Tyr		Leu Ile Glu His Gln		Arg Ile His Thr Gly Glu	
Lys Pro Tyr Arg		Cys Gly Gln Cys Gly		Lys Ser Phe Ile Lys Asn	
Ser Ser Leu Thr		Val His Gln Arg Ile		His Thr Gly Glu Lys Pro	
Tyr Arg Cys Gly		Glu Cys Gly Lys Thr		Phe Ser Arg Asn Thr Asn	
Leu Thr Arg His		Leu Arg Ile His Thr			

<210> 90

<211> 399

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4153521CD1

<400> 90

Met Ser Gln Val Thr	1	Phe Ser Asp Val Ala	10	Ile Asp Phe Ser His	15
	5		10		15
Glu Glu Trp Ala Cys	20	Leu Asp Ser Ala Gln	25	Arg Asp Leu Tyr Lys	30
	20		25		30
Asp Val Met Val Gln	35	Asn Tyr Glu Asn Leu	40	Val Ser Val Gly Leu	45
	35		40		45
Ser Val Thr Lys Pro	50	Tyr Val Ile Met Leu	55	Leu Glu Asp Gly Lys	60
	50		55		60
Glu Pro Trp Met Met		Glu Lys Lys Leu Ser		Lys Asp Trp Glu Ser	

				65					70					75
Arg	Trp	Glu	Asn	Lys	Glu	Leu	Ser	Thr	Lys	Lys	Asp	Ile	Tyr	Asp
				80					85					90
Glu	Asp	Ser	Pro	Gln	Pro	Val	Thr	Met	Glu	Lys	Val	Val	Lys	Gln
				95					100					105
Ser	Tyr	Glu	Phe	Ser	Asn	Ser	Asn	Lys	Asn	Leu	Glu	Tyr	Thr	Glu
				110					115					120
Cys	Asp	Thr	Phe	Arg	Ser	Thr	Phe	His	Ser	Lys	Ser	Thr	Leu	Ser
				125					130					135
Glu	Pro	Gln	Asn	Asn	Ser	Ala	Glu	Gly	Asn	Ser	His	Lys	Tyr	Asp
				140					145					150
Ile	Leu	Lys	Lys	Asn	Leu	Ser	Lys	Lys	Ser	Val	Ile	Lys	Ser	Glu
				155					160					165
Arg	Ile	Asn	Gly	Gly	Lys	Lys	Leu	Leu	Asn	Ser	Asn	Lys	Ser	Gly
				170					175					180
Ala	Ala	Phe	Asn	Gln	Ser	Lys	Ser	Leu	Thr	Leu	Pro	Gln	Thr	Cys
				185					190					195
Asn	Arg	Glu	Lys	Ile	Tyr	Thr	Cys	Ser	Glu	Cys	Gly	Lys	Ala	Phe
				200					205					210
Gly	Lys	Gln	Ser	Ile	Leu	Ser	Arg	His	Trp	Arg	Ile	His	Thr	Gly
				215					220					225
Glu	Lys	Pro	Tyr	Glu	Cys	Arg	Glu	Cys	Gly	Lys	Thr	Phe	Ser	His
				230					235					240
Gly	Ser	Ser	Leu	Thr	Arg	His	Gln	Ile	Ser	His	Ser	Gly	Glu	Lys
				245					250					255
Pro	Tyr	Lys	Cys	Ile	Glu	Cys	Gly	Lys	Ala	Phe	Ser	His	Gly	Ser
				260					265					270
Ser	Leu	Thr	Asn	His	Gln	Ser	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr
				275					280					285
Glu	Cys	Met	Asn	Cys	Gly	Lys	Ser	Phe	Ser	Arg	Val	Ser	Leu	Leu
				290					295					300
Ile	Gln	His	Leu	Arg	Ile	His	Thr	Gln	Glu	Lys	Arg	Tyr	Glu	Cys
				305					310					315
Arg	Ile	Cys	Gly	Lys	Ala	Phe	Ile	His	Ser	Ser	Ser	Leu	Ile	His
				320					325					330
His	Gln	Lys	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Arg	Glu
				335					340					345
Cys	Gly	Lys	Ala	Phe	Cys	Cys	Ser	Ser	His	Leu	Thr	Gln	His	Gln
				350					355					360
Arg	Ile	His	Ser	Met	Lys	Lys	Lys	Tyr	Glu	Cys	Asn	Lys	Cys	Leu
				365					370					375
Lys	Val	Phe	Ser	Ser	Phe	Ser	Phe	Leu	Val	Gln	His	Gln	Ser	Ile
				380					385					390
His	Thr	Glu	Glu	Lys	Pro	Phe	Glu	Val						
				395										

<210> 91

<211> 309

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4585038CD1

<400> 91

Met	Ala	Pro	Asn	Leu	Asp	Ser	Phe	Gly	Arg	Asp	Arg	Ala	Leu	Tyr
				5					10					15
Gln	Glu	His	Ala	Lys	Arg	Arg	Ile	Ala	Glu	Arg	Glu	Ala	Arg	Arg
				20					25					30
Thr	Arg	Arg	Arg	Gln	Ala	Arg	Glu	Gln	Thr	Gly	Lys	Met	Ala	Asp
				35					40					45
His	Leu	Glu	Gly	Leu	Ser	Ser	Asp	Asp	Glu	Glu	Thr	Ser	Thr	Asp

	50		55		60
Ile Thr Asn Phe	Asn Leu Glu Lys Asp Arg	Ile Ser Lys Glu Ser			
	65		70		75
Gly Lys Val Phe	Glu Asp Val Leu Glu Ser	Phe Tyr Ser Ile Asp			
	80		85		90
Cys Ile Lys Ser	Gln Phe Glu Ala Trp Arg	Ser Lys Tyr Tyr Thr			
	95		100		105
Ser Tyr Lys Asp	Ala Tyr Ile Gly Leu Cys	Leu Pro Lys Leu Phe			
	110		115		120
Asn Pro Leu Ile	Arg Leu Gln Leu Leu Thr	Trp Thr Pro Leu Glu			
	125		130		135
Ala Lys Cys Arg	Asp Phe Glu Asn Met	Leu Trp Phe Glu Ser			
	140		145		150
Leu Phe Tyr Gly	Cys Glu Glu Arg Glu	Gln Glu Lys Asp Asp			
	155		160		165
Asp Val Ala Leu	Leu Pro Thr Ile Val	Glu Lys Val Ile Leu			
	170		175		180
Lys Leu Thr Val	Ile Ala Glu Asn Met	Trp Asp Pro Phe Ser			
	185		190		195
Thr Gln Thr Ser	Arg Met Val Gly Ile	Thr Leu Lys Leu Ile			
	200		205		210
Gly Tyr Pro Ser	Val Val Asn Ala Glu	Asn Lys Asn Thr Gln			
	215		220		225
Tyr Leu Lys Ala	Leu Leu Leu Arg Met	Arg Arg Thr Leu Asp			
	230		235		240
Asp Val Phe Met	Pro Leu Tyr Pro Lys	Asn Val Leu Glu Asn			
	245		250		255
Asn Ser Gly Pro	Tyr Leu Phe Phe Gln	Arg Gln Phe Trp Ser			
	260		265		270
Val Lys Val Ile	Lys Pro Pro Phe Gln	Arg Gly Ser Cys Pro			
	275		280		285
Pro Arg Arg Lys	Glu Cys Cys Ser Glu	Arg Pro Arg Arg Ile			
	290		295		300
Thr Asp Arg Pro	Cys Val Val Phe Ser				
	305				

<210> 92

<211> 361

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4674640CD1

<400> 92

Met Ala Leu Asn	Val Ala Pro Val Arg	Asp Thr Lys Trp Leu	Thr	
1	5	10	15	
Leu Glu Val Cys	Arg Gln Phe Gln Arg	Gly Thr Cys Ser Arg	Ser	
	20	25	30	
Asp Glu Glu Cys	Lys Phe Ala His Pro	Pro Lys Ser Cys Gln	Val	
	35	40	45	
Glu Asn Gly Arg	Val Ile Ala Cys Phe	Asp Ser Leu Lys Gly	Arg	
	50	55	60	
Cys Ser Arg Glu	Asn Cys Lys Tyr Leu	His Pro Pro Thr His	Leu	
	65	70	75	
Lys Thr Gln Leu	Glu Ile Asn Gly Arg	Asn Asn Leu Ile Gln	Gln	
	80	85	90	
Lys Thr Ala Ala	Ala Met Leu Ala Gln	Gln Met Gln Phe Met	Phe	
	95	100	105	
Pro Gly Thr Pro	Leu His Pro Val Pro	Thr Phe Pro Val Gly	Pro	
	110	115	120	
Ala Ile Gly Thr	Asn Thr Ala Ile Ser	Phe Ala Pro Tyr Leu	Ala	

	125		130		135
Pro Val Thr Pro	Gly Val Gly Leu Val	Pro Thr Glu Ile Leu	Pro		
	140		145		150
Thr Thr Pro Val	Ile Val Pro Gly Ser	Pro Pro Val Thr Val	Pro		
	155		160		165
Gly Ser Thr Ala	Thr Gln Lys Leu Leu	Arg Thr Asp Lys Leu	Glu		
	170		175		180
Val Cys Arg Glu	Phe Gln Arg Gly Asn	Cys Ala Arg Gly Glu	Thr		
	185		190		195
Asp Cys Arg Phe	Ala His Pro Ala Asp	Ser Thr Met Ile Asp	Thr		
	200		205		210
Ser Asp Asn Thr	Val Thr Val Cys Met	Asp Tyr Ile Lys Gly	Arg		
	215		220		225
Cys Met Arg Glu	Lys Cys Lys Tyr Phe	His Pro Pro Ala His	Leu		
	230		235		240
Gln Ala Lys Ile	Lys Ala Ala Gln His	Gln Ala Asn Gln Ala	Ala		
	245		250		255
Val Ala Ala Gln	Ala Ala Ala Ala Ala	Ala Thr Val Met Ala	Phe		
	260		265		270
Pro Pro Gly Ala	Leu His Pro Leu Pro	Lys Arg Gln Ala Leu	Glu		
	275		280		285
Lys Ser Asn Gly	Thr Ser Ala Val Phe	Asn Pro Ser Val Leu	His		
	290		295		300
Tyr Gln Gln Ala	Leu Thr Ser Ala Gln	Leu Gln Gln His Ala	Ala		
	305		310		315
Phe Ile Pro Thr	Asp Asn Ser Glu Ile	Ile Ser Arg Asn Gly	Met		
	320		325		330
Glu Cys Gln Glu	Ser Ala Leu Arg Ile	Thr Lys His Cys Tyr	Cys		
	335		340		345
Thr Tyr Tyr Pro	Val Ser Ser Ser Ile	Glu Leu Pro Gln Thr	Ala		
	350		355		360

Cys

<210> 93

<211> 540

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4676066CD1

<400> 93

Met Pro Pro Cys	Ala Val Thr Pro Pro	Pro Pro Thr Ser Gln	Pro
1	5	10	15
Asn Trp Leu Thr	Leu Cys Leu Phe Pro	Ala Gly Gly Ser Ser	Gln
	20	25	30
Ile His Leu Ser	Asn Thr Glu Thr Ser	Gly Arg Pro Cys Thr	Arg
	35	40	45
Pro Pro Val Arg	Asp Pro Arg Gln Thr	Pro Ser Gln Pro Ala	Arg
	50	55	60
Pro Pro Gly Val	Gln Glu Arg His Gln	Pro Gly Leu Gln Ala	Pro
	65	70	75
Leu Ala Tyr Tyr	Gly Thr Ser Trp Pro	Leu Gln Ser His Leu	Met
	80	85	90
His Arg Tyr His	Ser Pro Val Thr Pro	Phe Ser Pro Leu Gln	Gly
	95	100	105
Leu Gly Pro Glu	Cys Arg Ser Val Ala	Ser Ala Arg Pro His	Thr
	110	115	120
His Gly Gly Cys	Cys Pro Gln Ala Glu	Gln Ser Lys Val Leu	Ser
	125	130	135
Ala Val Glu Asp	Arg Met Asp Glu Leu	Gly Ala Gly Ile Ala	Gln

	140		145		150
Ser Arg Arg Thr	Val Ala Leu Ile Lys	Ser Ala Ala Val Ala	Glu		
	155		160		165
Arg Glu Arg Val	Ser Arg Leu Phe Ala	Asp Ala Ala Ala Ala	Leu		
	170		175		180
Gln Gly Phe Gln	Thr Gln Val Leu Gly	Phe Ile Glu Glu Gly	Glu		
	185		190		195
Ala Ala Met Leu	Gly Arg Ser Gln Gly	Asp Leu Arg Arg Gln	Glu		
	200		205		210
Glu Gln Arg Ser	Arg Leu Ser Arg Ala	Arg Gln Asn Leu Ser	Gln		
	215		220		225
Val Pro Glu Ala	Asp Ser Val Ser Phe	Leu Gln Glu Leu Leu	Ala		
	230		235		240
Leu Arg Leu Ala	Leu Glu Asp Gly Cys	Gly Pro Gly Pro Gly	Pro		
	245		250		255
Pro Arg Glu Leu	Ser Phe Thr Lys Ser	Ser Gln Ala Val Arg	Ala		
	260		265		270
Val Arg Asp Met	Leu Ala Val Ala Cys	Val Asn Gln Trp Glu	Gln		
	275		280		285
Leu Arg Gly Pro	Gly Gly Asn Glu Asp	Gly Pro Gln Lys Leu	Asp		
	290		295		300
Ser Glu Ala Asp	Ala Glu Pro Gln Asp	Leu Glu Ser Thr Asn	Leu		
	305		310		315
Leu Glu Ser Glu	Ala Pro Arg Asp Tyr	Phe Leu Lys Phe Ala	Tyr		
	320		325		330
Ile Val Asp Leu	Asp Ser Asp Thr Ala	Asp Lys Phe Leu Gln	Leu		
	335		340		345
Phe Gly Thr Lys	Gly Val Lys Arg Val	Leu Cys Pro Ile Asn	Tyr		
	350		355		360
Pro Leu Ser Pro	Thr Arg Phe Thr His	Cys Glu Gln Val Leu	Gly		
	365		370		375
Glu Gly Ala Leu	Asp Arg Gly Thr Tyr	Tyr Trp Glu Val Glu	Ile		
	380		385		390
Ile Glu Gly Trp	Val Ser Met Gly Val	Met Ala Glu Asp Phe	Ser		
	395		400		405
Pro Gln Glu Pro	Tyr Asp Arg Gly Arg	Leu Gly Arg Asn Ala	His		
	410		415		420
Ser Cys Cys Leu	Gln Trp Asn Gly Arg	Ser Phe Ser Val Trp	Phe		
	425		430		435
His Gly Leu Glu	Ala Pro Leu Pro His	Pro Phe Ser Pro Thr	Val		
	440		445		450
Gly Val Cys Leu	Glu Tyr Ala Asp Arg	Ala Leu Ala Phe Tyr	Ala		
	455		460		465
Val Arg Asp Gly	Lys Met Ser Leu Leu	Arg Arg Leu Lys Ala	Ser		
	470		475		480
Arg Pro Arg Arg	Gly Gly Ile Pro Ala	Ser Pro Ile Asp Pro	Phe		
	485		490		495
Gln Ser Arg Leu	Asp Ser His Phe Ala	Gly Leu Phe Thr His	Arg		
	500		505		510
Leu Lys Pro Ala	Phe Phe Leu Glu Ser	Val Asp Ala His Leu	Gln		
	515		520		525
Ile Gly Pro Leu	Lys Lys Ser Cys Ile	Ser Val Leu Lys Arg	Arg		
	530		535		540

<210> 94

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4830687CD1

<400> 94

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Met Lys Val Lys Ile Lys Cys Trp Asn Gly Val Ala Thr Trp Leu
  1      5      10      15
Trp Val Ala Asn Asp Glu Asn Cys Gly Ile Cys Arg Met Ala Phe
      20      25      30
Asn Gly Cys Cys Pro Asp Cys Lys Val Pro Gly Asp Asp Cys Pro
      35      40      45
Leu Val Trp Gly Gln Cys Ser His Cys Phe His Met His Cys Ile
      50      55      60
Leu Lys Trp Leu His Ala Gln Gln Val Gln Gln His Cys Pro Met
      65      70      75
Cys Arg Gln Glu Trp Lys Phe Lys Glu
      80

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<210> 95

<211> 1312

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4880891CD1

<400> 95

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Met Lys Ala Leu Asp Glu Pro Pro Tyr Leu Thr Val Gly Thr Asp
  1      5      10      15
Val Ser Ala Lys Tyr Arg Gly Ala Phe Cys Glu Ala Lys Ile Lys
      20      25      30
Thr Ala Lys Arg Leu Val Lys Val Lys Val Thr Phe Arg His Asp
      35      40      45
Ser Ser Thr Val Glu Val Gln Asp Asp His Ile Lys Gly Pro Leu
      50      55      60
Lys Val Gly Ala Ile Val Glu Val Lys Asn Leu Asp Gly Ala Tyr
      65      70      75
Gln Glu Ala Val Ile Asn Lys Leu Thr Asp Ala Ser Trp Tyr Thr
      80      85      90
Val Val Phe Asp Asp Gly Asp Glu Lys Thr Leu Arg Arg Ser Ser
      95      100      105
Leu Cys Leu Lys Gly Glu Arg His Phe Ala Glu Ser Glu Thr Leu
      110      115      120
Asp Gln Leu Pro Leu Thr Asn Pro Glu His Phe Gly Thr Pro Val
      125      130      135
Ile Gly Lys Lys Thr Asn Arg Gly Arg Arg Ser Asn His Ile Pro
      140      145      150
Glu Glu Glu Ser Ser Ser Ser Ser Asp Glu Asp Glu Asp Asp
      155      160      165
Arg Lys Gln Ile Asp Glu Leu Leu Gly Lys Val Val Cys Val Asp
      170      175      180
Tyr Ile Ser Leu Asp Lys Lys Lys Ala Leu Trp Phe Pro Ala Leu
      185      190      195
Val Val Cys Pro Asp Cys Ser Asp Glu Ile Ala Val Lys Lys Asp
      200      205      210
Asn Ile Leu Val Arg Ser Phe Lys Asp Gly Lys Phe Thr Ser Val
      215      220      225
Pro Arg Lys Asp Val His Glu Ile Thr Ser Asp Thr Ala Pro Lys
      230      235      240
Pro Asp Ala Val Leu Lys Gln Ala Phe Glu Gln Ala Leu Glu Phe
      245      250      255
His Lys Ser Arg Thr Ile Pro Ala Asn Trp Lys Thr Glu Leu Lys
      260      265      270
Glu Asp Ser Ser Ser Ser Glu Ala Glu Glu Glu Glu Glu Glu
      275      280      285
Asp Asp Glu Lys Glu Lys Glu Asp Asn Ser Ser Glu Glu Glu Glu

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	290		295		300
Glu Ile Glu Pro	Phe Pro Glu Glu Arg	Glu Asn Phe Leu Gln	Gln		
	305		310		315
Leu Tyr Lys Phe	Met Glu Asp Arg Gly	Thr Pro Ile Asn Lys	Arg		
	320		325		330
Pro Val Leu Gly	Tyr Arg Asn Leu Asn Leu	Phe Lys Leu Phe	Arg		
	335		340		345
Leu Val His Lys	Leu Gly Gly Phe Asp	Asn Ile Glu Ser Gly	Ala		
	350		355		360
Val Trp Lys Gln	Val Tyr Gln Asp Leu	Gly Ile Pro Val Leu	Asn		
	365		370		375
Ser Ala Ala Gly	Tyr Asn Val Lys Cys	Ala Tyr Lys Lys Tyr	Leu		
	380		385		390
Tyr Gly Phe Glu	Glu Tyr Cys Arg Ser	Ala Asn Ile Glu Phe	Gln		
	395		400		405
Met Ala Leu Pro	Glu Lys Val Val Asn	Lys Gln Cys Lys Glu	Cys		
	410		415		420
Glu Asn Val Lys	Glu Ile Lys Val Lys	Glu Glu Asn Glu Thr	Glu		
	425		430		435
Ile Lys Glu Ile	Lys Met Glu Glu Glu	Arg Asn Ile Ile Pro	Arg		
	440		445		450
Glu Glu Lys Pro	Ile Glu Asp Glu Ile	Glu Arg Lys Glu Asn	Ile		
	455		460		465
Lys Pro Ser Leu	Gly Ser Lys Lys Asn	Leu Leu Glu Ser Ile	Pro		
	470		475		480
Thr His Ser Asp	Gln Glu Lys Glu Val	Asn Ile Lys Lys Pro	Glu		
	485		490		495
Asp Asn Glu Asn	Leu Asp Asp Lys Asp	Asp Asp Thr Thr Arg	Val		
	500		505		510
Asp Glu Ser Leu	Asn Ile Lys Val Glu	Ala Glu Glu Glu Lys	Ala		
	515		520		525
Lys Ser Gly Asp	Glu Thr Asn Lys Glu	Glu Asp Glu Asp Asp	Glu		
	530		535		540
Glu Ala Glu Glu	Glu Glu Glu Glu Glu	Glu Glu Glu Asp	Glu		
	545		550		555
Asp Asp Asp Asp	Asn Asn Glu Glu Glu	Glu Phe Glu Cys Tyr	Pro		
	560		565		570
Pro Gly Met Lys	Val Gln Val Arg Tyr	Gly Arg Gly Lys Asn	Gln		
	575		580		585
Lys Met Tyr Glu	Ala Ser Ile Lys Asp	Ser Asp Val Glu Gly	Gly		
	590		595		600
Glu Val Leu Tyr	Leu Val His Tyr Cys	Gly Trp Asn Val Arg	Tyr		
	605		610		615
Asp Glu Trp Ile	Lys Ala Asp Lys Ile	Val Arg Pro Ala Asp	Lys		
	620		625		630
Asn Val Pro Lys	Ile Lys His Arg Lys	Lys Ile Lys Asn Lys	Leu		
	635		640		645
Asp Lys Glu Lys	Asp Lys Asp Glu Lys	Tyr Ser Pro Lys Asn	Cys		
	650		655		660
Lys Leu Arg Arg	Leu Ser Lys Pro Pro	Phe Gln Thr Asn Pro	Ser		
	665		670		675
Pro Glu Met Val	Ser Lys Leu Asp Leu	Thr Asp Ala Lys Asn	Ser		
	680		685		690
Asp Thr Ala His	Ile Lys Ser Ile Glu	Ile Thr Ser Ile Leu	Asn		
	695		700		705
Gly Leu Gln Ala	Ser Glu Ser Ser Ala	Glu Asp Ser Glu Gln	Glu		
	710		715		720
Asp Glu Arg Gly	Ala Gln Asp Met Asp	Asn Asn Gly Lys Glu	Glu		
	725		730		735
Ser Lys Ile Asp	His Leu Thr Asn Asn	Arg Asn Asp Leu Ile	Ser		
	740		745		750
Lys Glu Glu Gln	Asn Ser Ser Ser Leu	Leu Glu Glu Asn Lys	Val		
	755		760		765

His	Ala	Asp	Leu	Val	Ile	Ser	Lys	Pro	Val	Ser	Lys	Ser	Pro	Glu
				770					775					780
Arg	Leu	Arg	Lys	Asp	Ile	Glu	Val	Leu	Ser	Glu	Asp	Thr	Asp	Tyr
				785					790					795
Glu	Glu	Asp	Glu	Val	Thr	Lys	Lys	Arg	Lys	Asp	Val	Lys	Lys	Asp
				800					805					810
Thr	Thr	Asp	Lys	Ser	Ser	Lys	Pro	Gln	Ile	Lys	Arg	Gly	Lys	Arg
				815					820					825
Arg	Tyr	Cys	Asn	Thr	Glu	Glu	Cys	Leu	Lys	Thr	Gly	Ser	Pro	Gly
				830					835					840
Lys	Lys	Glu	Glu	Lys	Ala	Lys	Asn	Lys	Glu	Ser	Leu	Cys	Met	Glu
				845					850					855
Asn	Ser	Ser	Asn	Ser	Ser	Ser	Asp	Glu	Asp	Glu	Glu	Glu	Thr	Lys
				860					865					870
Ala	Lys	Met	Thr	Pro	Thr	Lys	Lys	Tyr	Asn	Gly	Leu	Glu	Glu	Lys
				875					880					885
Arg	Lys	Ser	Leu	Arg	Thr	Thr	Gly	Phe	Tyr	Ser	Gly	Phe	Ser	Glu
				890					895					900
Val	Ala	Glu	Lys	Arg	Ile	Lys	Leu	Leu	Asn	Asn	Ser	Asp	Glu	Arg
				905					910					915
Leu	Gln	Asn	Ser	Arg	Ala	Lys	Asp	Arg	Lys	Asp	Val	Trp	Ser	Ser
				920					925					930
Ile	Gln	Gly	Gln	Trp	Pro	Lys	Lys	Thr	Leu	Lys	Glu	Leu	Phe	Ser
				935					940					945
Asp	Ser	Asp	Thr	Glu	Ala	Ala	Ala	Ser	Pro	Pro	His	Pro	Ala	Pro
				950					955					960
Glu	Glu	Gly	Val	Ala	Glu	Glu	Ser	Leu	Gln	Thr	Val	Ala	Glu	Glu
				965					970					975
Glu	Ser	Cys	Ser	Pro	Ser	Val	Glu	Leu	Glu	Lys	Pro	Pro	Pro	Val
				980					985					990
Asn	Val	Asp	Ser	Lys	Pro	Ile	Glu	Glu	Lys	Thr	Val	Glu	Val	Asn
				995					1000					1005
Asp	Arg	Lys	Ala	Glu	Phe	Pro	Ser	Ser	Gly	Ser	Asn	Ser	Val	Leu
				1010					1015					1020
Asn	Thr	Pro	Pro	Thr	Thr	Pro	Glu	Ser	Pro	Ser	Ser	Val	Thr	Val
				1025					1030					1035
Thr	Glu	Gly	Ser	Arg	Gln	Gln	Ser	Ser	Val	Thr	Val	Ser	Glu	Pro
				1040					1045					1050
Leu	Ala	Pro	Asn	Gln	Glu	Glu	Val	Arg	Ser	Ile	Lys	Ser	Glu	Thr
				1055					1060					1065
Asp	Ser	Thr	Ile	Glu	Val	Asp	Ser	Val	Ala	Gly	Glu	Leu	Gln	Asp
				1070					1075					1080
Leu	Gln	Ser	Glu	Gly	Asn	Ser	Ser	Pro	Ala	Gly	Phe	Asp	Ala	Ser
				1085					1090					1095
Val	Ser	Ser	Ser	Ser	Ser	Asn	Gln	Pro	Glu	Pro	Glu	His	Pro	Glu
				1100					1105					1110
Lys	Ala	Cys	Thr	Gly	Gln	Lys	Arg	Val	Lys	Asp	Ala	Gln	Gly	Gly
				1115					1120					1125
Gly	Ser	Ser	Ser	Lys	Lys	Gln	Lys	Arg	Ser	His	Lys	Ala	Thr	Val
				1130					1135					1140
Val	Asn	Asn	Lys	Lys	Lys	Gly	Lys	Gly	Thr	Asn	Ser	Ser	Asp	Ser
				1145					1150					1155
Glu	Glu	Leu	Ser	Ala	Gly	Glu	Ser	Ile	Thr	Lys	Ser	Gln	Pro	Val
				1160					1165					1170
Lys	Ser	Val	Ser	Thr	Gly	Met	Lys	Ser	His	Ser	Thr	Lys	Ser	Pro
				1175					1180					1185
Ala	Arg	Thr	Gln	Ser	Pro	Gly	Lys	Cys	Gly	Lys	Asn	Gly	Asp	Lys
				1190					1195					1200
Asp	Pro	Asp	Leu	Lys	Glu	Pro	Ser	Asn	Arg	Leu	Pro	Lys	Val	Tyr
				1205					1210					1215
Lys	Trp	Ser	Phe	Gln	Met	Ser	Asp	Leu	Glu	Asn	Met	Thr	Ser	Ala
				1220					1225					1230
Glu	Arg	Ile	Thr	Ile	Leu	Gln	Glu	Lys	Leu	Gln	Glu	Ile	Arg	Lys

	1235		1240		1245
His Tyr Leu Ser Leu Lys Ser Glu Val Ala Ser Ile Asp Arg Arg					
	1250		1255		1260
Arg Lys Arg Leu Lys Lys Glu Arg Glu Ser Ala Ala Thr Ser					
	1265		1270		1275
Ser Ser Ser Ser Ser Pro Ser Ser Ser Ser Ile Thr Ala Ala Val					
	1280		1285		1290
Met Leu Thr Leu Ala Glu Pro Ser Met Ser Ser Ala Ser Gln Asn					
	1295		1300		1305
Gly Met Ser Val Glu Cys Arg					
	1310				

<210> 96

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4909754CD1

<400> 96

Met Ala Trp Val Leu Lys Met Asp Glu Val Ile Glu Ser Gly Leu		
1 5 10 15		
Val His Asp Phe Asp Ala Ser Leu Ser Gly Ile Gly Gln Glu Leu		
20 25 30		
Gly Ala Gly Ala Tyr Ser Met Ser Asp Val Leu Ala Leu Pro Ile		
35 40 45		
Phe Lys Gln Glu Asp Ser Ser Leu Pro Leu Asp Gly Glu Thr Glu		
50 55 60		
His Pro Pro Phe Gln Tyr Val Met Cys Ala Ala Thr Ser Pro Ala		
65 70 75		
Val Lys Leu His Asp Glu Thr Leu Thr Tyr Leu Asn Gln Gly Gln		
80 85 90		
Ser Tyr Glu Ile Arg Met Leu Asp Asn Arg Lys Met Gly Asp Met		
95 100 105		
Pro Glu Ile Ser Gly Lys Leu Val Lys Ser Ile Ile Arg Val Val		
110 115 120		
Phe His Asp Arg Arg Leu Gln Tyr Thr Glu His Gln Gln Leu Glu		
125 130 135		
Gly Trp Lys Trp Asn Arg Pro Gly Asp Arg Leu Leu Asp Leu Asp		
140 145 150		
Ile Pro Met Ser Val Gly Ile Ile Asp Thr Arg Thr Asn Pro Ser		
155 160 165		
Gln Leu Asn Ala Val Glu Phe Leu Trp Asp Pro Ala Lys Arg Thr		
170 175 180		
Ser Ala Phe Ile Gln Val His Cys Ile Ser Thr Glu Phe Thr Pro		
185 190 195		
Arg Lys His Gly Gly Glu Lys Gly Val Pro Phe Arg Ile Gln Val		
200 205 210		
Asp Thr Phe Lys Gln Asn Glu Asn Gly Glu Tyr Thr Asp His Leu		
215 220 225		
His Ser Ala Ser Cys Gln Ile Lys Val Phe Lys Pro Lys Gly Ala		
230 235 240		
Asp Arg Lys Gln Lys Thr Asp Arg Glu Lys Met Glu Lys Arg Thr		
245 250 255		
Ala His Glu Lys Glu Lys Tyr Gln Pro Ser Tyr Asp Thr Thr Ile		
260 265 270		
Leu Thr Glu Cys Ser Pro Trp Pro Asp Ala Pro Thr Ala Tyr Val		
275 280 285		
Asn Asn Ser Pro Ser Pro Ala Pro Thr Phe Thr Ser Pro Gln Gln		
290 295 300		
Ser Thr Cys Ser Val Pro Asp Ser Asn Ser Ser Ser Pro Asn His		

	305		310		315
Gln Gly Asp Gly	Ala Ser Gln Thr Ser	Gly Glu Gln Ile Gln	Pro		
	320		325		330
Ser Ala Thr Ile	Gln Glu Thr Gln Gln Trp	Leu Leu Lys Asn	Arg		
	335		340		345
Phe Ser Ser Tyr	Thr Arg Leu Phe Ser	Asn Phe Ser Gly Ala	Asp		
	350		355		360
Leu Leu Lys Leu	Thr Lys Glu Asp Leu	Val Gln Ile Cys Gly	Ala		
	365		370		375
Ala Asp Gly Ile	Arg Leu Tyr Asn Ser	Leu Lys Ser Arg Ser	Val		
	380		385		390
Arg Pro Arg Leu	Thr Ile Tyr Val Cys	Arg Glu Gln Pro Ser	Ser		
	395		400		405
Thr Val Leu Gln	Gly Gln Gln Gln Ala	Ala Ser Ser Ala Ser	Glu		
	410		415		420
Asn Gly Ser Gly	Ala Pro Tyr Val Tyr	His Ala Ile Tyr Leu	Glu		
	425		430		435
Glu Met Ile Ala	Ser Glu Val Ala Arg	Lys Leu Ala Leu Val	Phe		
	440		445		450
Asn Ile Pro Leu	His Gln Ile Asn Gln	Val Tyr Arg Gln Gly	Pro		
	455		460		465
Thr Gly Ile His	Ile Leu Val Ser Asp	Gln Met Val Gln Asn	Phe		
	470		475		480
Gln Asp Glu Ser	Cys Phe Leu Phe Ser	Thr Val Lys Ala Glu	Ser		
	485		490		495
Ser Asp Gly Ile	His Ile Ile Leu Lys				
	500				

<210> 97

<211> 227

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4911931CD1

<400> 97

Met Phe Lys Arg	Met Ala Glu Phe Gly	Pro Asp Ser Gly Gly	Arg
1	5	10	15
Val Lys Gly Val	Thr Ile Val Lys Pro	Ile Val Tyr Gly Asn	Val
	20	25	30
Ala Arg Tyr Phe	Gly Lys Lys Arg Glu	Glu Asp Gly His Thr	His
	35	40	45
Gln Trp Thr Val	Tyr Val Lys Pro Tyr	Arg Asn Glu Asp Met	Ser
	50	55	60
Ala Tyr Val Lys	Lys Ile Gln Phe Lys	Leu His Glu Ser Tyr	Gly
	65	70	75
Asn Pro Leu Arg	Val Val Thr Lys Pro	Pro Tyr Glu Ile Thr	Glu
	80	85	90
Thr Gly Trp Gly	Glu Phe Glu Ile Ile	Ile Lys Ile Phe Phe	Ile
	95	100	105
Asp Pro Asn Glu	Arg Pro Val Thr Leu	Tyr His Leu Leu Lys	Leu
	110	115	120
Phe Gln Ser Asp	Thr Asn Ala Met Leu	Gly Lys Lys Thr Val	Val
	125	130	135
Ser Glu Phe Tyr	Asp Glu Met Ile Phe	Gln Asp Pro Thr Ala	Met
	140	145	150
Met Gln Gln Leu	Leu Thr Thr Ser Arg	Gln Leu Thr Leu Gly	Ala
	155	160	165
Tyr Lys His Glu	Thr Glu Phe Ala Glu	Leu Glu Val Lys Thr	Arg
	170	175	180
Glu Lys Leu Glu	Ala Ala Lys Lys Lys	Thr Ser Phe Glu Ile	Ala

	185		190		195
Glu Leu Lys Glu Arg Leu Lys Ala Ser Arg Glu Thr Ile Asn Cys					
	200		205		210
Leu Lys Asn Glu Ile Arg Lys Leu Glu Glu Asp Asp Gln Ala Lys					
	215		220		225
Asp Ile					

<210> 98
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4920433CD1

<400> 98

Met Ala Glu Asp Gly Leu Pro Lys Ile Tyr Ser His Pro Pro Thr		
1 5 10 15		
Glu Ser Ser Lys Thr Pro Thr Ala Ala Thr Ile Phe Phe Gly Ala		
20 25 30		
Asp Asn Ala Ile Pro Lys Ser Glu Thr Thr Ile Thr Ser Glu Gly		
35 40 45		
Asp His Val Thr Ser Val Asn Glu Tyr Met Leu Glu Ser Asp Phe		
50 55 60		
Ser Thr Thr Thr Asp Asn Lys Leu Thr Ala Lys Lys Glu Lys Leu		
65 70 75		
Lys Ser Glu Asp Asp Met Gly Thr Asp Phe Ile Lys Ser Thr Thr		
80 85 90		
His Leu Gln Lys Glu Ile Thr Ser Leu Thr Gly Thr Thr Asn Ser		
95 100 105		
Ile Thr Arg Asp Ser Ile Thr Glu His Phe Met Pro Val Lys Ile		
110 115 120		
Gly Asn Ile Ser Ser Pro Val Thr Thr Val Ser Leu Ile Asp Phe		
125 130 135		
Ser Thr Asp Ile Ala Lys Glu Asp Ile Leu Leu Ala Thr Ile Asp		
140 145 150		
Thr Gly Asp Ala Glu Ile Ser Ile Thr Ser Glu Val Ser Gly Thr		
155 160 165		
Leu Lys Asp Ser Ser Ala Gly Val Ala Asp Ala Pro Ala Phe Pro		
170 175 180		
Arg Lys Lys Asp Glu Ala Asp Met Ser Asn Tyr Asn Ser Ser Ile		
185 190 195		
Lys Ser Asn Val Pro Ala Asp Glu Ala Val Gln Val Thr Asp Ser		
200 205 210		
Ile Ile Pro Glu Ala Glu Ile Leu Leu Leu Leu Lys Lys Pro His		
215 220 225		
Tyr Tyr Ser Arg His Asn Cys Pro		
230		

<210> 99
 <211> 511
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 5042113CD1

<400> 99

Met Asp Glu Glu Ser Leu Glu Ser Ala Leu Gln Thr Tyr Arg Ala		
1 5 10 15		

Gln	Leu	Gln	Gln	Val	Glu	Leu	Ala	Leu	Gly	Ala	Gly	Leu	Asp	Ser	
				20					25					30	
Ser	Glu	Gln	Ala	Asp	Leu	Arg	Gln	Leu	Gln	Gly	Asp	Leu	Lys	Glu	
				35					40					45	
Leu	Ile	Glu	Leu	Thr	Glu	Ala	Ser	Leu	Val	Ser	Val	Arg	Lys	Ser	
				50					55					60	
Arg	Leu	Leu	Ala	Ala	Leu	Asp	Glu	Glu	Arg	Pro	Gly	Arg	Gln	Glu	
				65					70					75	
Asp	Ala	Glu	Tyr	Gln	Ala	Phe	Arg	Glu	Ala	Ile	Thr	Glu	Ala	Val	
				80					85					90	
Glu	Ala	Pro	Ala	Ala	Ala	Arg	Gly	Ser	Gly	Ser	Glu	Thr	Val	Pro	
				95					100					105	
Lys	Ala	Glu	Ala	Gly	Pro	Glu	Ser	Ala	Ala	Gly	Gly	Gln	Glu	Glu	
				110					115					120	
Glu	Glu	Gly	Glu	Asp	Glu	Glu	Glu	Leu	Ser	Gly	Thr	Lys	Val	Ser	
				125					130					135	
Ala	Pro	Tyr	Tyr	Ser	Ser	Trp	Gly	Thr	Leu	Glu	Tyr	His	Asn	Ala	
				140					145					150	
Met	Val	Val	Gly	Thr	Glu	Glu	Ala	Glu	Asp	Gly	Ser	Ala	Gly	Val	
				155					160					165	
Arg	Val	Leu	Tyr	Leu	Tyr	Pro	Thr	His	Lys	Ser	Leu	Lys	Pro	Cys	
				170					175					180	
Pro	Phe	Phe	Leu	Glu	Gly	Lys	Cys	Arg	Phe	Lys	Glu	Asn	Cys	Arg	
				185					190					195	
Phe	Ser	His	Gly	Gln	Val	Val	Ser	Leu	Asp	Glu	Leu	Arg	Pro	Phe	
				200					205					210	
Gln	Asp	Pro	Asp	Leu	Ser	Ser	Leu	Gln	Ala	Gly	Ser	Ala	Cys	Leu	
				215					220					225	
Ala	Lys	His	Gln	Asp	Gly	Leu	Trp	His	Ala	Ala	Arg	Ile	Thr	Asp	
				230					235					240	
Val	Asp	Asn	Gly	Tyr	Tyr	Thr	Val	Lys	Phe	Asp	Ser	Leu	Leu	Leu	
				245					250					255	
Arg	Glu	Ala	Val	Val	Glu	Gly	Asp	Gly	Ile	Leu	Pro	Pro	Leu	Arg	
				260					265					270	
Thr	Glu	Ala	Thr	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Gly	Thr	Gly	Asp	
				275					280					285	
Ser	Ser	Tyr	Ala	Arg	Val	Val	Gly	Ser	Asp	Ala	Val	Asp	Ser	Gly	
				290					295					300	
Thr	Cys	Ser	Ser	Ala	Phe	Ala	Gly	Trp	Glu	Val	His	Thr	Arg	Gly	
				305					310					315	
Ile	Gly	Ser	Arg	Leu	Leu	Thr	Lys	Met	Gly	Tyr	Glu	Phe	Gly	Lys	
				320					325					330	
Gly	Leu	Gly	Arg	His	Ala	Glu	Gly	Arg	Val	Glu	Pro	Ile	His	Ala	
				335					340					345	
Val	Val	Leu	Pro	Arg	Gly	Lys	Ser	Leu	Asp	Gln	Cys	Val	Glu	Thr	
				350					355					360	
Leu	Gln	Lys	Gln	Thr	Arg	Val	Gly	Lys	Ala	Gly	Thr	Asn	Lys	Pro	
				365					370					375	
Pro	Arg	Cys	Arg	Gly	Arg	Gly	Ala	Arg	Pro	Gly	Gly	Arg	Pro	Ala	
				380					385					390	
Pro	Arg	Asn	Val	Phe	Asp	Phe	Leu	Asn	Glu	Lys	Leu	Gln	Gly	Gln	
				395					400					405	
Ala	Pro	Gly	Ala	Leu	Glu	Ala	Gly	Ala	Ala	Pro	Ala	Gly	Arg	Arg	
				410					415					420	
Ser	Lys	Asp	Met	Tyr	His	Ala	Ser	Lys	Ser	Ala	Lys	Arg	Ala	Leu	
				425					430					435	
Ser	Leu	Arg	Leu	Phe	Gln	Thr	Glu	Glu	Lys	Ile	Glu	Arg	Thr	Gln	
				440					445					450	
Arg	Asp	Ile	Arg	Ser	Ile	Gln	Glu	Ala	Leu	Ala	Arg	Asn	Ala	Gly	
				455					460					465	
Arg	His	Ser	Val	Ala	Ser	Ala	Gln	Leu	Gln	Glu	Lys	Leu	Ala	Gly	
				470					475					480	
Ala	Gln	Arg	Gln	Leu	Gly	Gln	Leu	Arg	Ala	Gln	Glu	Ala	Gly	Leu	

	485		490		495
Gln Gln Glu Gln Arg Lys Ala Asp Thr His Lys Lys Met Thr Glu					
	500		505		510
Phe					

<210> 100

<211> 247

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5083853CD1

<400> 100

Met Glu Val Leu Glu Ser Gly Glu Gln Gly Val Leu Gln Trp Asp	
1 5 10 15	
Arg Lys Leu Ser Glu Leu Ser Glu Pro Gly Asp Gly Glu Ala Leu	
20 25 30	
Met Tyr His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln	
35 40 45	
Asn Val Leu Gly Gln Leu Leu Asn Asp Pro Phe Leu Ser Glu Lys	
50 55 60	
Ser Val Ser Met Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro	
65 70 75	
Leu Ile Gln Ala Glu His Ser Tyr Ser Leu Cys Glu Glu Pro Arg	
80 85 90	
Ala Gln Ser Pro Phe Thr His Ile Thr Ser Asp Ser Phe Asn Asp	
95 100 105	
Asp Glu Val Glu Ser Glu Lys Trp Tyr Leu Ser Thr Asp Phe Pro	
110 115 120	
Ser Thr Ser Ile Lys Thr Glu Pro Ile Thr Asp Glu Pro Pro Pro	
125 130 135	
Gly Leu Val Pro Ser Val Thr Leu Thr Ile Thr Ala Ile Ser Thr	
140 145 150	
Pro Leu Glu Lys Glu Glu Pro Pro Leu Glu Met Asn Thr Gly Val	
155 160 165	
Asp Ser Ser Cys Gln Thr Ile Ile Pro Lys Ile Lys Leu Glu Pro	
170 175 180	
His Glu Val Asp Gln Phe Leu Asn Phe Ser Pro Lys Glu Gly Leu	
185 190 195	
Ser Ala Leu Pro Val Ser Leu Trp Val Met Asp Met Val Ser Gly	
200 205 210	
Ser Thr Glu Arg Glu Tyr Gly Glu Arg Ala Gly Met Ser Leu Tyr	
215 220 225	
His Arg Cys Cys Ser Trp Leu Tyr Glu Ile Ala Leu Phe Leu Lys	
230 235 240	
Asn Lys Asn Phe Ala Ser Lys	
245	

<210> 101

<211> 276

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5283981CD1

<400> 101

Met Gly Ser Lys Ala Leu Pro Ala Pro Ile Pro Leu His Pro Ser	
1 5 10 15	


```

Leu Gln Leu Thr Asn Tyr Ser Phe Leu Gln Ala Val Asn Thr Phe
      20      25      30
Pro Ala Thr Val Asp His Leu Gln Gly Leu Tyr Gly Leu Ser Ala
      35      40      45
Val Gln Thr Met His Met Asn His Trp Thr Leu Gly Tyr Pro Asn
      50      55      60
Val His Glu Ile Thr Arg Ser Thr Ile Thr Glu Met Ala Ala Ala
      65      70      75
Gln Gly Leu Val Asp Ala Arg Phe Pro Phe Pro Ala Leu Pro Phe
      80      85      90
Thr Thr His Leu Phe His Pro Lys Gln Gly Ala Ile Ala His Val
      95     100     105
Leu Pro Ala Leu His Lys Asp Arg Pro Arg Phe Asp Phe Ala Asn
     110     115     120
Leu Ala Val Ala Ala Thr Gln Glu Asp Pro Pro Lys Met Gly Asp
     125     130     135
Leu Ser Lys Leu Ser Pro Gly Leu Gly Ser Pro Ile Ser Gly Leu
     140     145     150
Ser Lys Leu Thr Pro Asp Arg Lys Pro Ser Arg Gly Arg Leu Pro
     155     160     165
Ser Lys Thr Lys Lys Glu Phe Ile Cys Lys Phe Cys Gly Arg His
     170     175     180
Phe Thr Lys Ser Tyr Asn Leu Leu Ile His Glu Arg Thr His Thr
     185     190     195
Asp Glu Arg Pro Tyr Thr Cys Asp Ile Cys His Lys Ala Phe Arg
     200     205     210
Arg Gln Asp His Leu Arg Asp His Arg Tyr Ile His Ser Lys Glu
     215     220     225
Lys Pro Phe Lys Cys Gln Glu Cys Gly Lys Gly Phe Cys Gln Ser
     230     235     240
Arg Thr Leu Ala Val His Lys Thr Leu His Met Gln Thr Ser Ser
     245     250     255
Pro Thr Ala Ala Ser Ser Ala Ala Lys Cys Ser Gly Glu Thr Val
     260     265     270
Ile Cys Gly Gly Thr Ala
      275

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<210> 102

<211> 220

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5510549CD1

<400> 102

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Met Pro Leu Gln Arg Leu Asp Asn Asp Val Asp Leu Arg Gly Asp
  1      5      10      15
Gln Pro Ser Leu Gly Ser Phe Thr Tyr Ser Thr Ser Ala Pro Gly
     20      25      30
Pro Ala Leu Ser Pro Ser Val Pro Leu His Tyr Leu Pro His Asp
     35      40      45
Pro Leu His Gln Glu Leu Ser Phe Gly Val Pro Tyr Ser His Met
     50      55      60
Met Pro Arg Arg Leu Ser Thr Gln Arg Tyr Arg Leu Gln Gln Pro
     65      70      75
Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Tyr Tyr Pro
     80      85      90
Ser Phe Leu Pro Tyr Phe Leu Ser Met Leu Pro Met Ser Pro Thr
     95     100     105
Ala Met Gly Pro Thr Ile Ser Leu Asp Leu Asp Val Asp Asp Val
    110     115     120

```

Glu Met Glu Asn Tyr Glu Ala Leu Leu Asn Leu Ala Glu Arg Leu	
	125 130 135
Gly Asp Ala Lys Pro Arg Gly Leu Thr Lys Ala Asp Ile Glu Gln	
	140 145 150
Leu Pro Ser Tyr Arg Phe Asn Pro Asp Ser His Gln Ser Glu Gln	
	155 160 165
Thr Leu Cys Val Val Cys Phe Ser Asp Phe Glu Ala Arg Gln Leu	
	170 175 180
Leu Arg Val Leu Pro Cys Asn His Glu Phe His Thr Lys Cys Val	
	185 190 195
Asp Lys Trp Leu Lys Ala Asn Arg Thr Cys Pro Ile Cys Arg Ala	
	200 205 210
Asp Ala Ser Glu Val Pro Arg Glu Ala Glu	
	215 220

<210> 103
 <211> 608
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 5544862CD1

<400> 103

Met Asp Thr Glu Glu Arg Lys Asp Lys Asp Ser Ile His Gly His	
1 5 10 15	
Ser Gln Leu Asp Lys Arg Pro Glu Pro Ser Thr Leu Glu Asn Ile	
20 25 30	
Thr Asp Asp Lys Tyr Ala Thr Val Ser Ser Pro Ser Lys Ser Lys	
35 40 45	
Lys Leu Glu Cys Pro Ser Pro Ala Glu Gln Lys Pro Ala Glu His	
50 55 60	
Val Ser Leu Ser Asn Pro Ala Pro Leu Leu Val Ser Pro Glu Val	
65 70 75	
His Leu Thr Pro Ala Val Pro Ser Leu Pro Ala Thr Val Pro Ala	
80 85 90	
Trp Pro Ser Glu Pro Thr Thr Phe Gly Pro Thr Gly Val Pro Ala	
95 100 105	
Pro Ile Pro Val Leu Ser Val Thr Gln Thr Leu Thr Thr Gly Pro	
110 115 120	
Asp Ser Ala Val Ser Gln Ala His Leu Thr Pro Ser Pro Val Pro	
125 130 135	
Val Ser Ile Gln Ala Val Asn Gln Pro Leu Met Pro Leu Pro Gln	
140 145 150	
Thr Leu Ser Leu Tyr Gln Asp Pro Leu Tyr Pro Gly Phe Pro Cys	
155 160 165	
Asn Glu Lys Gly Asp Arg Ala Ile Val Pro Pro Tyr Ser Leu Cys	
170 175 180	
Gln Thr Gly Glu Asp Leu Pro Lys Asp Lys Asn Ile Leu Arg Phe	
185 190 195	
Phe Phe Asn Leu Gly Val Lys Ala Tyr Ser Cys Pro Met Trp Ala	
200 205 210	
Pro His Ser Tyr Leu Tyr Pro Leu His Gln Ala Tyr Leu Ala Ala	
215 220 225	
Cys Arg Met Tyr Pro Lys Val Pro Val Pro Val Tyr Pro His Asn	
230 235 240	
Pro Trp Phe Gln Glu Ala Pro Ala Ala Gln Asn Glu Ser Asp Cys	
245 250 255	
Thr Cys Thr Asp Ala His Phe Pro Met Gln Thr Glu Ala Ser Val	
260 265 270	
Asn Gly Gln Met Pro Gln Pro Glu Ile Gly Pro Pro Thr Phe Ser	
275 280 285	

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Ser Pro Leu Val Ile Pro Pro Ser Gln Val Ser Glu Ser His Gly
290 295 300
Gln Leu Ser Tyr Gln Ala Asp Leu Glu Ser Glu Thr Pro Gly Gln
305 310 315
Leu Leu His Ala Asp Tyr Glu Glu Ser Leu Ser Gly Lys Asn Met
320 325 330
Phe Pro Gln Pro Ser Phe Gly Pro Asn Pro Phe Leu Gly Pro Val
335 340 345
Pro Ile Ala Pro Pro Phe Phe Pro His Val Trp Tyr Gly Tyr Pro
350 355 360
Phe Gln Gly Phe Ile Glu Asn Pro Val Met Arg Gln Asn Ile Val
365 370 375
Leu Pro Ser Asp Glu Lys Gly Glu Leu Asp Leu Ser Leu Glu Asn
380 385 390
Leu Asp Leu Ser Lys Asp Cys Gly Ser Val Ser Thr Val Asp Glu
395 400 405
Phe Pro Glu Ala Arg Gly Glu His Val His Ser Leu Pro Glu Ala
410 415 420
Ser Val Ser Ser Lys Pro Asp Glu Gly Arg Thr Glu Gln Ser Ser
425 430 435
Gln Thr Arg Lys Ala Asp Thr Ala Leu Ala Ser Ile Pro Pro Val
440 445 450
Ala Glu Gly Lys Ala His Pro Pro Thr Gln Ile Leu Asn Arg Glu
455 460 465
Arg Glu Thr Val Pro Val Glu Leu Glu Pro Lys Arg Thr Ile Gln
470 475 480
Ser Leu Lys Glu Lys Lys Lys Lys Val Lys Asp Pro Lys Thr Ala
485 490 495
Ala Asp Val Val Ser Pro Gly Ala Asn Ser Val Asp Ser Arg Val
500 505 510
Gln Arg Pro Lys Glu Glu Ser Ser Glu Asp Glu Asn Glu Val Ser
515 520 525
Asn Ile Leu Arg Ser Gly Arg Ser Lys Gln Phe Tyr Asn Gln Thr
530 535 540
Tyr Gly Ser Arg Lys Tyr Lys Ser Asp Trp Gly Tyr Ser Gly Arg
545 550 555
Gly Gly Tyr Gln His Val Arg Ser Glu Glu Ser Trp Lys Gly Gln
560 565 570
Pro Ser Arg Ser Arg Asp Glu Gly Tyr Gln Tyr His Arg Asn Val
575 580 585
Arg Gly Arg Pro Phe Arg Gly Asp Arg Arg Arg Ser Gly Met Gly
590 595 600
Asp Gly His Arg Gly Gln His Thr
605

```

<210> 104

<211> 653

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5573394CD1

<400> 104

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Met Glu Trp Asp Lys Gln Gly Cys Thr Gly Lys Leu Gln Arg Ala
1 5 10 15
Ile Val Ser Ile Leu Asn Tyr Val Ile Tyr Lys Asn Thr His Ile
20 25 30
Lys Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile Phe Gln Phe
35 40 45
Pro Leu Asn Leu Cys Thr Lys Thr Ile Val Glu Thr Ile Arg Val
50 55 60

```

Ser	Leu	Gln	Gly	Lys	Pro	Met	Met	Ser	Asn	Leu	Lys	Glu	Ile	His
				65					70					75
Leu	Val	Ser	Asn	Glu	Asp	Pro	Thr	Val	Ala	Ala	Phe	Lys	Ala	Ala
				80					85					90
Ser	Glu	Phe	Ile	Leu	Gly	Lys	Ser	Glu	Leu	Gly	Gln	Glu	Thr	Thr
				95					100					105
Pro	Ser	Phe	Asn	Ala	Met	Val	Val	Asn	Asn	Leu	Thr	Leu	Gln	Ile
				110					115					120
Val	Gln	Gly	His	Ile	Glu	Trp	Gln	Thr	Ala	Asp	Val	Ile	Val	Asn
				125					130					135
Ser	Val	Asn	Pro	His	Asp	Ile	Thr	Val	Gly	Pro	Val	Ala	Lys	Ser
				140					145					150
Ile	Leu	Gln	Gln	Ala	Gly	Val	Glu	Met	Lys	Ser	Glu	Phe	Leu	Ala
				155					160					165
Thr	Lys	Ala	Lys	Gln	Phe	Gln	Arg	Ser	Gln	Leu	Val	Leu	Val	Thr
				170					175					180
Lys	Gly	Phe	Asn	Leu	Phe	Cys	Lys	Tyr	Ile	Tyr	His	Val	Leu	Trp
				185					190					195
His	Ser	Glu	Phe	Pro	Lys	Pro	Gln	Ile	Leu	Lys	His	Ala	Met	Lys
				200					205					210
Glu	Cys	Leu	Glu	Lys	Cys	Ile	Glu	Gln	Asn	Ile	Thr	Ser	Ile	Ser
				215					220					225
Phe	Pro	Ala	Leu	Gly	Thr	Gly	Asn	Met	Glu	Ile	Lys	Lys	Glu	Thr
				230					235					240
Ala	Ala	Glu	Ile	Leu	Phe	Asp	Glu	Val	Leu	Thr	Phe	Ala	Lys	Asp
				245					250					255
His	Val	Lys	His	Gln	Leu	Thr	Val	Lys	Phe	Val	Ile	Phe	Pro	Thr
				260					265					270
Asp	Leu	Glu	Ile	Tyr	Lys	Ala	Phe	Ser	Ser	Glu	Met	Ala	Lys	Arg
				275					280					285
Ser	Lys	Met	Leu	Ser	Leu	Asn	Asn	Tyr	Ser	Val	Pro	Gln	Ser	Thr
				290					295					300
Arg	Glu	Glu	Lys	Arg	Glu	Asn	Gly	Leu	Glu	Ala	Arg	Ser	Pro	Ala
				305					310					315
Ile	Asn	Leu	Met	Gly	Phe	Asn	Val	Glu	Glu	Met	Cys	Glu	Ala	His
				320					325					330
Ala	Trp	Ile	Gln	Arg	Ile	Leu	Ser	Leu	Gln	Asn	His	His	Ile	Ile
				335					340					345
Glu	Asn	Asn	His	Ile	Leu	Tyr	Leu	Gly	Arg	Lys	Glu	His	Asp	Ile
				350					355					360
Leu	Ser	Gln	Leu	Gln	Lys	Thr	Ser	Ser	Val	Ser	Ile	Thr	Glu	Ile
				365					370					375
Ile	Ser	Pro	Gly	Arg	Thr	Glu	Leu	Glu	Ile	Glu	Gly	Ala	Arg	Ala
				380					385					390
Asp	Leu	Ile	Glu	Val	Val	Met	Asn	Ile	Glu	Asp	Met	Leu	Cys	Lys
				395					400					405
Val	Gln	Glu	Glu	Met	Ala	Arg	Lys	Lys	Glu	Arg	Gly	Leu	Trp	Arg
				410					415					420
Ser	Leu	Gly	Gln	Trp	Thr	Ile	Gln	Gln	Lys	Thr	Gln	Asp	Glu	
				425					430					435
Met	Lys	Glu	Asn	Ile	Ile	Phe	Leu	Lys	Cys	Pro	Val	Pro	Pro	Thr
				440					445					450
Gln	Glu	Leu	Leu	Asp	Gln	Lys	Lys	Gln	Phe	Glu	Lys	Cys	Gly	Leu
				455					460					465
Gln	Val	Leu	Lys	Val	Glu	Lys	Ile	Asp	Asn	Glu	Val	Leu	Met	Ala
				470					475					480
Ala	Phe	Gln	Arg	Lys	Lys	Lys	Met	Met	Glu	Glu	Lys	Leu	His	Arg
				485					490					495
Gln	Pro	Val	Ser	His	Arg	Leu	Phe	Gln	Gln	Val	Pro	Tyr	Gln	Phe
				500					505					510
Cys	Asn	Val	Val	Cys	Arg	Val	Gly	Phe	Gln	Arg	Met	Tyr	Ser	Thr
				515					520					525
Pro	Cys	Asp	Pro	Lys	Tyr	Gly	Ala	Gly	Ile	Tyr	Phe	Thr	Lys	Asn

	530		535		540
Leu Lys Asn Leu	Ala Glu Lys Ala Lys	Lys Ile Ser Ala Ala	Asp		
	545		550		555
Lys Leu Ile Tyr	Val Phe Glu Ala Glu	Val Leu Thr Gly Phe	Phe		
	560		565		570
Cys Gln Gly His	Pro Leu Asn Ile Val	Pro Pro Pro Leu Ser	Pro		
	575		580		585
Gly Ala Ile Asp	Gly His Asp Ser Val	Val Asp Asn Val Ser	Ser		
	590		595		600
Pro Glu Thr Phe	Val Ile Phe Ser Gly	Met Gln Ala Ile Pro	Gln		
	605		610		615
Tyr Leu Trp Thr	Cys Thr Gln Glu Tyr	Val Gln Ser Gln Asp	Tyr		
	620		625		630
Ser Ser Gly Pro	Met Arg Pro Phe Ala	Gln His Pro Trp Arg	Gly		
	635		640		645
Phe Ala Ser Gly	Ser Pro Val Asp				
	650				

<210> 105

<211> 154

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5850840CD1

<400> 105

Met Gly Asn Cys	Leu Lys Ser Pro Thr	Ser Asp Asp Ile Ser	Leu
1	5	10	15
Leu His Glu Ser	Gln Ser Asp Arg Ala	Ser Phe Gly Glu Gly	Thr
	20	25	30
Glu Pro Asp Gln	Glu Pro Pro Pro Pro	Tyr Gln Glu Gln Val	Pro
	35	40	45
Val Pro Val Tyr	His Pro Thr Pro Ser	Gln Thr Arg Leu Ala	Thr
	50	55	60
Gln Leu Thr Glu	Glu Glu Gln Ile Arg	Ile Ala Gln Arg Ile	Gly
	65	70	75
Leu Ile Gln His	Leu Pro Lys Gly Val	Tyr Asp Pro Gly Arg	Asp
	80	85	90
Gly Ser Glu Lys	Lys Ile Arg Glu Cys	Val Ile Cys Met Met	Asp
	95	100	105
Phe Val Tyr Gly	Asp Pro Ile Arg Phe	Leu Pro Cys Met His	Ile
	110	115	120
Tyr His Leu Asp	Cys Ile Asp Asp Trp	Leu Met Arg Ser Phe	Thr
	125	130	135
Cys Pro Ser Cys	Met Glu Pro Val Asp	Ala Ala Leu Leu Ser	Ser
	140	145	150
Tyr Glu Thr Asn			

<210> 106

<211> 337

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5942936CD1

<400> 106

Met Lys Arg Pro	Cys Glu Glu Thr Thr	Ser Glu Ser Asp Met	Asp
1	5	10	15

```

Glu Thr Ile Asp Val Gly Ser Glu Asn Asn Tyr Ser Gly Gln Ser
    20                25                30
Thr Ser Ser Val Ile Arg Leu Asn Ser Pro Thr Thr Thr Ser Gln
    35                40                45
Ile Met Ala Arg Lys Lys Arg Arg Gly Ile Ile Glu Lys Arg Arg
    50                55                60
Arg Asp Arg Ile Asn Asn Ser Leu Ser Glu Leu Arg Arg Leu Val
    65                70                75
Pro Thr Ala Phe Glu Lys Gln Gly Ser Ala Lys Leu Glu Lys Ala
    80                85                90
Glu Ile Leu Gln Met Thr Val Asp His Leu Lys Met Leu Gln Ala
    95                100               105
Thr Gly Gly Lys Gly Tyr Phe Asp Ala His Ala Leu Ala Met Asp
   110               115               120
Phe Met Ser Ile Gly Phe Arg Glu Cys Leu Thr Glu Val Ala Arg
   125               130               135
Tyr Leu Ser Ser Val Glu Gly Leu Asp Ser Ser Asp Pro Leu Arg
   140               145               150
Val Arg Leu Val Ser His Leu Ser Thr Cys Ala Thr Gln Arg Glu
   155               160               165
Ala Ala Ala Met Thr Ser Ser Met Ala His His His His Pro Leu
   170               175               180
His Pro His His Trp Ala Ala Ala Phe His His Leu Pro Ala Ala
   185               190               195
Leu Leu Gln Pro Asn Gly Leu His Ala Ser Glu Ser Thr Pro Cys
   200               205               210
Arg Leu Ser Thr Thr Ser Glu Val Pro Pro Ala His Gly Ser Ala
   215               220               225
Leu Leu Thr Ala Thr Phe Ala His Ala Asp Ser Ala Leu Arg Met
   230               235               240
Pro Ser Thr Gly Ser Val Ala Pro Cys Val Pro Pro Leu Ser Thr
   245               250               255
Ser Leu Leu Ser Leu Ser Ala Thr Val His Ala Ala Ala Ala Ala
   260               265               270
Ala Thr Ala Ala Ala His Ser Phe Pro Leu Ser Phe Ala Gly Ala
   275               280               285
Phe Pro Met Leu Pro Pro Asn Ala Ala Ala Ala Val Ala Ala Ala
   290               295               300
Thr Ala Ile Ser Pro Pro Leu Ser Val Ser Ala Thr Ser Ser Pro
   305               310               315
Gln Gln Thr Ser Ser Gly Thr Asn Asn Lys Pro Tyr Arg Pro Trp
   320               325               330
Gly Thr Glu Val Gly Ala Phe
   335

```

<210> 107

<211> 535

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5951431CD1

<400> 107

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Met Ala Ala Glu Pro Asn Lys Thr Glu Ile Gln Thr Leu Phe Lys
  1          5          10          15
Arg Leu Arg Ala Val Pro Thr Asn Lys Ala Cys Phe Asp Cys Gly
  20          25          30
Ala Lys Asn Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu
  35          40          45
Cys Ile Asp Cys Ser Gly Val His Arg Ser Leu Gly Val His Leu
  50          55          60

```

Ser	Phe	Ile	Arg	Ser	Thr	Glu	Leu	Asp	Ser	Asn	Trp	Asn	Trp	Phe	
				65					70					75	
Gln	Leu	Arg	Cys	Met	Gln	Val	Gly	Gly	Asn	Ala	Asn	Ala	Thr	Ala	
				80					85					90	
Phe	Phe	Arg	Gln	His	Gly	Cys	Thr	Ala	Asn	Asp	Ala	Asn	Thr	Lys	
				95					100					105	
Tyr	Asn	Ser	Arg	Ala	Ala	Gln	Met	Tyr	Arg	Glu	Lys	Ile	Arg	Gln	
				110					115					120	
Leu	Gly	Ser	Ala	Ala	Leu	Ala	Arg	His	Gly	Thr	Asp	Leu	Trp	Ile	
				125					130					135	
Asp	Asn	Met	Ser	Ser	Ala	Val	Pro	Asn	His	Ser	Pro	Glu	Lys	Lys	
				140					145					150	
Asp	Ser	Asp	Phe	Phe	Thr	Glu	His	Thr	Gln	Pro	Pro	Ala	Trp	Asp	
				155					160					165	
Ala	Pro	Ala	Thr	Glu	Pro	Ser	Gly	Thr	Gln	Gln	Pro	Ala	Pro	Ser	
				170					175					180	
Thr	Glu	Ser	Ser	Gly	Leu	Ala	Gln	Pro	Glu	His	Gly	Pro	Asn	Thr	
				185					190					195	
Asp	Leu	Leu	Gly	Thr	Ser	Pro	Lys	Ala	Ser	Leu	Glu	Ser	Val	Tyr	
				200					205					210	
Leu	Ser	Ala	Lys	Gly	Ala	Leu	Pro	Ala	Arg	Glu	Leu	Lys	Ser	Ser	
				215					220					225	
Ile	Ile	Gly	Lys	Lys	Lys	Pro	Ala	Ala	Ala	Lys	Lys	Gly	Leu	Gly	
				230					235					240	
Ala	Lys	Lys	Gly	Leu	Gly	Ala	Gln	Lys	Val	Ser	Ser	Gln	Ser	Phe	
				245					250					255	
Ser	Glu	Ile	Glu	Arg	Gln	Ala	Gln	Val	Ala	Glu	Lys	Leu	Arg	Glu	
				260					265					270	
Gln	Gln	Ala	Ala	Asp	Ala	Lys	Lys	Gln	Ala	Glu	Glu	Ser	Met	Val	
				275					280					285	
Ala	Ser	Met	Arg	Leu	Ala	Tyr	Gln	Glu	Leu	Gln	Ile	Asp	Arg	Lys	
				290					295					300	
Lys	Glu	Glu	Lys	Lys	Leu	Gln	Asn	Leu	Glu	Gly	Lys	Lys	Arg	Glu	
				305					310					315	
Gln	Ala	Glu	Arg	Leu	Gly	Met	Gly	Leu	Val	Ser	Arg	Ser	Ser	Val	
				320					325					330	
Ser	His	Ser	Val	Leu	Ser	Glu	Met	Gln	Val	Ile	Glu	Gln	Glu	Thr	
				335					340					345	
Pro	Val	Ser	Ala	Lys	Ser	Ser	Arg	Ser	Gln	Leu	Asp	Leu	Phe	Asp	
				350					355					360	
Asp	Val	Gly	Thr	Phe	Ala	Ser	Gly	Pro	Pro	Lys	Tyr	Lys	Asp	Asn	
				365					370					375	
Pro	Phe	Ser	Leu	Gly	Glu	Ser	Phe	Gly	Ser	Arg	Trp	Asp	Thr	Asp	
				380					385					390	
Ala	Ala	Trp	Gly	Met	Asp	Arg	Val	Glu	Glu	Lys	Glu	Pro	Glu	Val	
				395					400					405	
Thr	Ile	Ser	Ser	Ile	Arg	Pro	Ile	Ser	Glu	Arg	Ala	Thr	Asn	Arg	
				410					415					420	
Arg	Glu	Val	Glu	Ser	Arg	Ser	Ser	Gly	Leu	Glu	Ser	Ser	Glu	Ala	
				425					430					435	
Arg	Gln	Lys	Phe	Ala	Gly	Ala	Lys	Ala	Ile	Ser	Ser	Asp	Met	Phe	
				440					445					450	
Phe	Gly	Arg	Glu	Val	Asp	Ala	Glu	Tyr	Glu	Ala	Arg	Ser	Arg	Leu	
				455					460					465	
Gln	Gln	Leu	Ser	Gly	Ser	Ser	Ala	Ile	Ser	Ser	Ser	Asp	Leu	Phe	
				470					475					480	
Gly	Asp	Met	Asp	Gly	Ala	His	Gly	Ala	Gly	Ser	Val	Ser	Leu	Gly	
				485					490					495	
Asn	Val	Leu	Pro	Thr	Ala	Asp	Ile	Ala	Gln	Phe	Lys	Gln	Gly	Val	
				500					505					510	
Lys	Ser	Val	Ala	Gly	Lys	Met	Ala	Val	Leu	Ala	Asn	Gly	Val	Met	
				515					520					525	
Asn	Ser	Leu	Gln	Asp	Arg	Tyr	Gly	Ser	Tyr						

530

535

<210> 108
<211> 2173
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 095210CB1

<400> 108
cggcgccct gtccccgtaa ctgtgacacg ggtgcacgag agcgtcattg ggggcatgg 60
gggcccgtgct ggggtgcgct ttgcaccagt gacgcagccg ctgcatctcc gccagtccgc 120
gcaggccagc atccttcaga aaaagcatcc ccgaggagga agacgaatcg ttaaacatct 180
gaaaggggtca ggccagcatc cttcagaaaa agcatccccg aggaggaaga cgaatcgta 240
aacatcttag gtcagctcta gcctctcgga atttgtcttc ttcagtggaa accccgagaa 300
gactgatcag ttcttcagtt ctaaaaaat ggcccagggt ttggtgacgt tcgccgacgt 360
agccatagac ttttctcagg aggagtgggc ctgtctgaac tctgctcaga gggacctgta 420
ctgggacgtg atgctggaga actacagtaa cttggtctca ctggatttgg agtcagcata 480
tgaaaaataag agtttaccta cagaaaaaaa cattcatgaa ataagggtt ccaaaaggaa 540
ttcagataga agaagtaaat cccttgccg taactggata tgtgaaggta cgcttgaaag 600
accacagcgc tccagaggga ggtatgtcaa tcagatgatc atcaattatg tcaaaaggcc 660
tgctactaga gaaggcacc ctcctagaac acatcagaga catcataagg agaattcctt 720
tgaatgtaag gactgtggga aggccttag tctgtgctat caacttagtc aacatcagaa 780
aatccatact ggtgagaaac cttatgaatg taaagaatgt aagaaggcct tccgttgggg 840
caatcagctt actcaacatc aaaaaattca tactggggag aagccctacg aatgtaaaga 900
ctgtgggaag gcttttcgat ggggtcaag cctcgattat cataagagga ttcatactgg 960
tgaaaaaacc tatgaatgta aagactgtgg aaaggccttt cggcgtggtg atgagctcac 1020
tcagcaccag agattccaca ctggggagaa agactacgaa tgcaaagact gtgggaagac 1080
ctttagccgt gtgtataaac ttattcagca caagagaatt catagtgggg agaagcctta 1140
cgagtgtaaa gactgtggga aggcctttat ttgtgttca agcctcattc agcataaaag 1200
aattcacaca ggtgagaaac cctatgaatg tcaagaatgt ggaaggcct ttactcgagt 1260
caattacctt actcagcatc agaagatcca caccgtgag aagcctcacg aatgtaagga 1320
gtgtgggaag gcctttcgct ggggttcgag cctcgttaag cacgagagga tacatacggg 1380
cgagaagccg tacaagtgc cagaatgtgg gaaggccttc aattgtgggt atcacctcac 1440
tcagcagcag agaatccaca caggcgaaac cccgtataaa tgtaaggagt gtgggaaggc 1500
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<223> Incyte ID No: 159196CB1

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<213> Homo sapiens

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<223> Incyte ID No: 343338CB1

<400> 111

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<210> 112

<211> 2181

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 402386CB1

<400> 112

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<211> 2400

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<213> Homo sapiens

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<400> 113

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<211> 1440

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 490256CB1

<400> 114

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<210> 115

<211> 2238

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 494740CB1

<220>

<221> unsure

<222> 10, 49, 60, 127

<223> a, t, c, g, or other

<400> 115

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gggggcccagn tctctctccg agttccttaa tccggggccg tcaattaana tccggggccn 60
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ctgggcnгаа gaaggggggg ccctcattcg ggacctgca ctccgtcgcc ggaagtgcc 180
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```

```

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```

<210> 116

<211> 873

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 507475CB1

<400> 116

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ctaggtcctg ggacagaata gttacgacct ctgggacagg aactcttctc tcttttggtta 240
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tatgtcgtg gaggaaggc ctgagtcca gggacctgtg gttgacaggc gctgccctcg 540
atgtggtcat gaaggaatgg cataccacac cagacagatg cgttcagccg atgaagggca 600
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ttcctgggca actctacagt ccctccctcc tttcgggaagg tgaaggatac tgggttttta 720
gatgccttgt ccactctgtc tgggtgcaat gttttgtccc cagaagagaa tcagatcatc 780
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gttatatttt tctataagac cctgaaaaaa aaa 873

```

<210> 117

<211> 2826

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 531581CB1

<400> 117

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gggtaaaatt ccattctgat atcaaaatgc agtattcgca ccactgtgag caccttttag 120
agagactgaa caaacagcg gaagcaggtt ttctctgtga ctgtaccata gtgattgggg 180
aatccagtt taaagctcat aggaatgtgc tggcctcctt tagtgagtat tttggtgcga 240
tctacagaag cacttctgag aacaatgtct ttcttgatca gattcaggtg aaggctgatg 300
gatttcagaa actgttggag tttatatata caggaaactt aaactctgac agttggaatg 360

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```

ttaaagaaat tcatcaggct gctgactatc tcaaagtgga agagggtggc actaaatgca 420
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ttactggaaa cattgaattg aatcaacaga cttgtcttct tactctgcga gattataata 540
atcgagagaa atcagaagta tctacagatt tgattcaggc aaatcctaaa caaggcgcgt 600
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tgaggaaaat gtacttgagt tttgaaatat tttgtaagc ctctcttact cctgttatgc 2760
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ctagaa 2826

```

<210> 118

<211> 859

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 675190CB1

<400> 118

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acttgggttc tggcctatag gaacaagaca ttttcagtaa tggaaagaagg agcttccagg 180
ctggggaaga tcatcatttc cagtggtagc ttgacctgag atgataacct accaccactt 240
ctgggaaggc ccagaataga cagaagagag agaacatact agagttgcta gcccctaaga 300
gttgaacgaa atgggcaagg cccagctgaa ataacaggaa acacatgaaa aatgccacga 360
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aagatgtggc tgtgggcttc accaggagg agtggcagtt tttggaccag tctcagaagg 480
tcttgtaaca ggaagtaatg ttggagaact acatcaacct agtatcaata ggggtatcgag 540
gcaccaagcc agattcgcct tccaagttgy agcaaggaga acccccaggg atagcagaag 600

```

```

gagcagccca cagtcaaadc tgtccagggt attcattcag gagaaggacc ctacagatgg 660
agggaaatgca ggaaagctaa gaagaatcac acctcattgc agatctgcat taccgttgga 720
aaacagcagc ctcagaacca cagtagccat gaagaccatc agccttcaac caccaccctt 780
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cattatatat cttgtcttc                                     859

```

<210> 119

<211> 1652

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 685434CB1

<400> 119

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accaacaaaa agtcagcaca aagtgaactt tactgagtat tataatcagc tcttttggaat 180
gccagttttt catagtata ttaagatatg gttgttaaata tagatcacia aaattgcttt 240
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cttgtggaac ttggatctag ttgggaaggc aagactaatc atacatgcaa cagtgaagaa 540
taatttaacg cccagacccc tctacatccc acgggaacag aagtactgtc agctttgaag 600
gagaaggcct catggaggag ctgtgacttg actccagagt gaaaggataa ttaggattga 660
tacaggacgg aggaaggaag gcatccaggc aatctcaata aaagttaggt gctcaggagg 720
agatgctcta tctggctact cgtatcgaac aagaaaatgt tatcaatcac acggatgaag 780
aaggatttac tcctctgatg tgggctgcag cacacgggca aatagctgtg gtagagttcc 840
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gtctttgtat caagtgtgt aatttgacat tttcagaaat tattctacct tagtcatctt 1500
cactcgtgta ttaagtcatt caotttatat agggtttgct ataaatccct agaaaaaaat 1560
tgttcttatt gttgaataaa aaagtgcaca gtgtgattgt ttacaaaatg atattataaa 1620
taataaaaat acttcttctg tcaaaaaaaa aa                                     1652

```

<210> 120

<211> 1612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 788663CB1

<400> 120

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tcctacagac acggcagtg aaaggaaaaa aaagtactga cttacagtga tttagcaaac 420
actgcacagc aatcagaaac ttttcagttt cttgcagata tattacaaa gaagatttta 480

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```

gctagtaaat acctgaaaaat gcttaaagag gaaaagaggg aagaagatga ggagaatgac 540
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agcctggcga ggacagccct ggaccactc cactgtctct aagtaaaccac agcactgccc 660
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```

<210> 121

<211> 1975

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 870100CB1

<400> 121

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<213> Homo sapiens

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<223> Incyte ID No: 1234329CB1

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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1238747CB1

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<210> 127

<211> 1588

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 1265980CB1

<400> 127

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<210> 128

<211> 2205

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 1297333CB1

<400> 128

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<210> 129

<211> 2735

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 1312824CB1

<400> 129

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<210> 130

<211> 3174

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1359294CB1

<400> 130

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<210> 131

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<212> DNA

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<223> Incyte ID No: 1377380CB1

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<210> 132

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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1383473CB1

<400> 132

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<210> 133

<211> 1894

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
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<210> 134
 <211> 1927
 <212> DNA
 <213> Homo sapiens

<220>
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<211> 1895

<212> DNA

<213> Homo sapiens

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<400> 135

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<211> 1180

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<213> Homo sapiens

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 <213> Homo sapiens

<220>
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 <223> Incyte ID No: 1483455CB1

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<210> 139

<211> 1678

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1527064CB1

<400> 139

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<211> 2060

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 1557491CB1

<400> 140

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<210> 141

<211> 3270

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 1576862CB1

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<210> 142
<211> 1907
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 1609731CB1

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<210> 143

<211> 1800

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1674538CB1

<400> 143

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<210> 144

<211> 1848

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1675287CB1

<400> 144

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<210> 145

<211> 2056

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1693903CB1

<400> 145

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<210> 146

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1702962CB1

<400> 146

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<210> 147

<211> 1114

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1712916CB1

<400> 147

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<210> 148

<211> 2380

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1748313CB1

<400> 148

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<210> 149
<211> 1628
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 1754833CB1

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<210> 150
<211> 2210
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 1798701CB1

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<400> 150

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<210> 151

<211> 1220

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1842496CB1

<400> 151

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<210> 152

<211> 1687

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1868613CB1

<400> 152

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<210> 153

<211> 2797

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1870609CB1

<400> 153

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<210> 154

<211> 2685

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1871961CB1

<400> 154

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ggcatcccca  ggcctcgag  cccccagcct  cacaccccca  caactggcca  ctccaaattt  540
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<210> 155

<211> 1879

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1876258CB1

<400> 155

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<210> 156

<211> 4462

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1929822CB1

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<210> 157

<211> 2203

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1970095CB1

<400> 157

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<210> 158

<211> 1393

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1975473CB1

<400> 158

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cgccacatt ggccccttcc aggccctgc ttgtcccaa agcggacggc tctcaccccc 180
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<210> 159

<211> 2164

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1976527CB1

<400> 159

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aaaa 2164

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<210> 160

<211> 445

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2108023CB1

<400> 160

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tcattgtagc tccagataag gaatatcttc tgatcgtcat tcagaatcca tgtgaataga 360
cctgcgatgg ccaaggctgt ttaagcgaca ctgggttggg aacacttggc tctctcatga 420
gtattaaaat tctatttcaa tctaa 445

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<210> 161

<211> 2029

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2135746CB1

<400> 161

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<210> 162

<211> 1813

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 2154810CB1

<400> 162

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gagacctcaa gaaggatact tcagtagtgt gaaaatgcc a tctgaaaagg tgtcctctta 600
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<210> 163

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2228991CB1

<400> 163

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<210> 164

<211> 1852

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2241206CB1

<400> 164

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ttggaacatg gatagccgct tgcaggagat ccgggagcgg cagaagttac ggcgacagct 180
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<210> 165

<211> 960

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2259590CB1

<400> 165

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ggccttggcg acagcctgtg tcctcacggc gcgcagaggc ggcgcgcgca acctgtgtgt 240
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<210> 166

<211> 2718

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2307537CB1

<400> 166

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agagacaaac actgaactaa aagaaagggg aaaggagctg tctgagggga tagttgatga 180
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<210> 167

<211> 1884

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2440675CB1

<400> 167

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cggcagaacc caggcgaggg acagctccgg acaggtgtgg ggtgcacact gaaaatgcca 180
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gagaaactgg cagttattgc tgtcaaaagc ctgttctctc aactgctgtc aataaaatta 1860
aagatacaga aaaaaaaaaa aaaa 1884

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<210> 168

<211> 2317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2463542CB1

<400> 168

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aattaattta gcttctttga aatgattagg tcaacttttg gtttaaaaga ttaccatggg 180
tgtcccaaaa atctttgcat gtaccaattt atttctcct ccctagggtc agaagtattt 240
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<210> 169

<211> 1760

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2486031CB1

<400> 169

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<210> 170

<211> 1965

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2493052CB1

<400> 170

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<210> 171

<211> 2086

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2512074CB1

<400> 171

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<210> 172

<211> 1461

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 2646274CB1

<400> 172

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acattgtaag ttccagttct ggccggggcg ggtggctcac acctgtaatc ccagcacttt 180
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actggtggaa aaatttccat ttgttcgaaa atcagagaga aactggaat gttacgttca 360
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tattgaaaaa ctactcaagc tggatgtgaa tgcattcccg cagggtattg aagatgctga 480
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<210> 173

<211> 1066

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2672566CB1

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ctgttgacat ggaaaacaag gaaaatggct ctgtcgggtg aaaaaattcc atggaaaatg 180
ggagaccacc tgatcctgca gactgggccg tgatggatgt cgtcaattat ttccgaaccg 240
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<210> 174

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2689674CB1

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cagagccttt gccaccatgg gggagacctt aatgagcgtc aaaattatcc gaaaccgcct 360
cactgggatc ccagctggct actgcttgtt agaatttgca gatttggcca cagctgagaa 420
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actgaactat gccacttacg ggaaacaacc agataacagc cctgagtatt cctcttttgt 540
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<210> 175

<211> 2155

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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aggacctttc cgaagcgctg agtggcctaa cggtcacagc tgtcgcccat cggagaggca 120
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<210> 176

<211> 1687

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2738293CB1

<400> 176

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1687

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<210> 177

<211> 744

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2772776CB1

<400> 177

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ggccatgatc gggcccgggg gcctgagcct gggacccac cccgtgttaa tgaaaaatga 720
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744

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<210> 178

<211> 1127

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2774476CB1

<400> 178

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<210> 179

<211> 1408

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2804624CB1

<400> 179

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<210> 180

<211> 1685

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2848225CB1

<400> 180

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ggcagaggga ggacctgga acatcccga agccgggaaa tggacgcagt ggcctttgag 180
gatgtggctg tgaacttcac ccaggaggaa tgggctttgc tgggtccatc acagaagaat 240
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gtagagagat tcagtgaag taaagacagt agtcagtgtg gagaaacatt tagcctcatt 420
cgagatagta ttgtgaacaa cagcatttgt cctggagaag atccatgtca aagcgctgag 480
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cacaaccac atgagtatca ggaatatgga gagaagccac atacacataa acaacgtggg 600
aaagccttca gttaccatca ctctttcag tcgcgtggaa ggcctcacac tggaaagaaa 660
cgctatgagt gtaaggaaat tggaaaaacc ttcagttctc gtagaaacct tcgaagacac 720
atggtagtgc aaggtggaaa tagacctat aagtgttaagt tgtgtgggaa agcttttttt 780
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aagcagtgtt ctaaagcctt tcctttttac agttcctatc gaagacatga gagaatgcac 900
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<210> 181
<211> 1166
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 2882241CB1

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<400> 181
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gccggcacc taggccggcc cgccgccagc tgtcgccgac atggaaccct tggccagcaa 180
catccaggtc ctgctgcagg cggccgagtt cctggagcgc cgtgagagag aggccgagca 240
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gcgcaggagg gccagttga agcgggtgcct ggagcggctg aagcagcaga tgcccctggg 420
ggccgactgt gcccggtaca ccacgctgag cctgtgcgc cgtgccagga tgcacatcca 480
gaagctggag gatcaggagc agcggggccg acagctcaag gagaggctgc gcagcaagca 540
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```

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<210> 182
<211> 1958
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: 2939011CB1

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<400> 182
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tgtgcaacaa ggtttgttta tcgatggaca cttttacaac aggatttatg aagctgggtc 300
ggagaacaac acggcagttg tagcagtaga aactcacacg atacacaaaa ttgaagaagg 360

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gattgatata ggcactatag aagcaaatga ggatatggaa attgcttacc ccataacttg 420
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gtgtgtcaag ttcaatgatc agttgatcag ccccaagcac tttgttcac tggctggcaa 540
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gccaggagtt atgttttgat ttggaatttt aattatttgt ttatttttat cattgtccca 1920
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<210> 183

<211> 2679

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2947188CB1

<400> 183

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aattggccct agggcagcag gaacctattg tttcagaagt cgggtacctt tgaggacgtg 180
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gaaacagact tttcagaagc ctctcttcta gagaacaac aggaagtcca ctacgagga 540
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gaaaagatga aaaataaaga tttatttaat ccattccaca 2679

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<210> 184

<211> 810

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3094001CB1

<400> 184

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caaagacctg tttgatctga tcctcacttg cgaagagaga gtgtatgacc aggtggtgga 420
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aggagatgcc aaaacgccag atgaaagcaa 810

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<210> 185

<211> 2233

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3110061CB1

<400> 185

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ctggcgagg ccttgctgat gaacctgact gagggtcctt ggcatggca gaaatggacc 60
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agcagcaaat tggagaaaaat ctttccagag gggatgattg gataccttca tttgggaaga 480
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<210> 186

<211> 2187

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3146614CB1

<400> 186

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<211> 1556

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3295381CB1

<400> 187

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<210> 188

<211> 2032

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3364774CB1


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<210> 189

<211> 1882

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3397777CB1

<400> 189

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<211> 784

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3403046CB1

<400> 190

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<211> 1771

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 3538506CB1

<400> 191

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<211> 1764

<212> DNA

<213> Homo sapiens

<220>

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<400> 192

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<211> 2923

<212> DNA

<213> Homo sapiens

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<211> 1567

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<213> Homo sapiens

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<210> 196

<211> 1817

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 3892962CB1

<400> 196

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<210> 197

<211> 2836

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4153521CB1

<400> 197

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<210> 198

<211> 1434

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 4585038CB1

<400> 198

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<210> 199

<211> 2445

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4674640CB1

<400> 199

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<211> 2099

<212> DNA

<213> Homo sapiens

<220>

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